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(54) Title: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAS ENCODING THESE PROTEINS

(57) Abstract

The present invention provides human proteins having hydrophobic domains, DNAs coding for these proteins, and expression vectors for these DNAs as well as eucaryotic cells expressing these DNAs.

DESCRIPTION

Human Proteins Having Hydrophobic Domains and DNAs Encoding These Proteins

TECHNICAL FIELD

The present invention relates to human proteins having hydrophobic domains, DNAs coding for these proteins, and expression vectors for these DNAs as well as eucaryotic cells expressing these DNAs. The proteins of the present invention can be employed as pharmaceuticals or as antigens for preparing antibodies against these proteins. The human cDNAs of the present invention can be utilized as probes for the genetic diagnosis and gene sources for the gene therapy. Furthermore, the cDNAs can be utilized as gene sources for large-scale production of the proteins encoded by these cDNAs. Cells into which these genes are introduced to express secretory proteins and membrane proteins in large amounts can be utilized for detection of the corresponding receptors and ligands, screening of novel low-molecular pharmaceuticals, and so on.

BACKGROUND ART

Cells secrete many proteins outside the cells. These secretory proteins play important roles for the proliferation control, the differentiation induction, the material transportation, the biological protection, etc. in the cells. Different from intracellular proteins, the secretory proteins exert their actions outside the cells, whereby they can be administered in the intracorporeal manner such as the injection or the drip, so that there are

hidden potentialities as medicines. In fact, a number of human secretory proteins such as interferons, interleukins, erythropoietin, thrombolytic agents, etc. have been currently employed as medicines. In addition, secretory proteins other than those described above have been undergoing clinical trials to develop as pharmaceuticals. Because it has been conceived that the human cells still produce many unknown secretory proteins, availability of these secretory proteins as well as genes coding for them is expected to lead to development of novel pharmaceuticals utilizing these proteins.

On the other hand, membrane proteins play important roles, as signal receptors, ion channels, transporters, etc. in the material transportation and the information transmission through the cell membrane. Examples thereof include receptors for a variety of cytokines, ion channels for the sodium ion, the potassium ion, the chloride ion, etc., transporters for saccharides and amino acids, and so on, where the genes for many of them have been cloned already. It has been clarified that abnormalities of these membrane proteins are associated with a number of hitherto-cryptogenic diseases. Therefore, discovery of a new membrane protein is anticipated to lead to elucidation of the causes of many diseases, so that isolation of a new gene coding for the membrane protein has been desired.

Heretofore, owing to difficulty in the purification from human cells, these secretory proteins and membrane proteins have been isolated by an approach from the gene side. A general method is the so-called expression cloning which comprises introduction of a cDNA library into eucaryotic cells to express cDNAs and then screening of the cells secreting, or expressing on the surface of membrane,

the objective active protein. However, this method is applicable only to cloning of a gene for a protein with a known function.

In general, secretory proteins and membrane proteins possess at least one hydrophobic domain inside the proteins, wherein, after synthesis thereof in the ribosome, this domain works as a secretory signal or remains in the phospholipid membrane to be trapped in the membrane. Accordingly, the evidence of this cDNA for encoding a secretory protein and a membrane protein is provided by determination of the whole base sequence of a full-length cDNA followed by detection of highly hydrophobic domain(s) in the amino acid sequence of the protein encoded by this cDNA.

OBJECTS OF THE INVENTION

The main object of the present invention is to provide novel human proteins having hydrophobic domains, DNAs coding for these proteins, and expression vectors for these DNAs as well as transformed eucaryotic cells that are capable of expressing these DNAs. This object as well as other objects and advantages of the present invention will become apparent to those skilled in the art from the following description with reference to the accompanying drawings.

BRIEF DESCRIPTION OF DRAWINGS

Fig. 1 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01550.

Fig. 2 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02593.

Fig. 3 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10195.

Fig. 4 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10423.

Fig. 5 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10506.

Fig. 6 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10507.

Fig. 7 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10548.

Fig. 8 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10566.

Fig. 9 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10567.

Fig. 10 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10568.

Fig. 11 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01426.

Fig. 12 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02515.

Fig. 13 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02575.

Fig. 14 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10357.

Fig. 15 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10447.

Fig. 16 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10477.

Fig. 17 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10513.

Fig. 18 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10540.

Fig. 19 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10557.

Fig. 20 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10563.

Fig. 21 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01467.

Fig. 22 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01956.

Fig. 23 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02545.

Fig. 24 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02551.

Fig. 25 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02631.

Fig. 26 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02632.

Fig. 27 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10488.

Fig. 28 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10538.

Fig. 29 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10542.

Fig. 30 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10571.

Fig. 31 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01470.

Fig. 32 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02419.

Fig. 33 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02631.

Fig. 34 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02695.

Fig. 35 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10031.

Fig. 36 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10530.

Fig. 37 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10541.

Fig. 38 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10550.

Fig. 39 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10590.

Fig. 40 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10591.

Fig. 41 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01462.

Fig. 42 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02485.

Fig. 43 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02798.

Fig. 44 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10041.

Fig. 45 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10246.

Fig. 46 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10392.

Fig. 47 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10489.

Fig. 48 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10519.

Fig. 49 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10531.

Fig. 50 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10574.

SUMMARY OF THE INVENTION

As the result of intensive studies, the present inventors have been successful in cloning of cDNAs coding for proteins having hydrophobic domains from the human full-length cDNA bank, thereby completing the present invention. In other words, the present invention provides human proteins having hydrophobic domains, namely proteins comprising any of the amino acid sequences represented by SEQ ID Nos. 1 to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130. Moreover, the present invention provides DNAs coding for the above-mentioned proteins, exemplified by cDNAs comprising any of the base sequences represented by SEQ ID Nos. 11 to 20, 41 to 50, 71 to 80, 101 to 110, and 131 to 140, as well as expression vectors that are capable of expressing any of these DNAs by in vitro translation or in eucaryotic cells and transformed eucaryotic cells that are capable of expressing these DNAs and of producing the above-mentioned proteins.

DETAILED DESCRIPTION OF THE INVENTION

The proteins of the present invention can be obtained, for example, by a method for isolation from human organs, cell lines, etc., a method for preparation of peptides by the chemical synthesis, or a method for production with the recombinant DNA technology using the DNAs coding for the hydrophobic domains of the present invention, among which the method for production with the recombinant DNA technology is employed preferably. For instance, in vitro expression of the proteins can be achieved by preparation of an RNA by in vitro transcription from a vector having one of the cDNAs of the present invention, followed by in vitro translation using this RNA as a template. Also, introduction of the translated region into a suitable expression vector

by the method known in the art leads to expression of a large amount of the encoded protein in prokaryotic cells such as *Escherichia coli*, *Bacillus subtilis*, etc., and eucaryotic cells such as yeasts, insect cells, mammalian cells, etc.

In the case where one of the proteins of the present invention is produced by expressing the DNA by in vitro translation, the protein of the present invention can be produced in vitro, when the translated region of this cDNA is introduced into a vector having an RNA polymerase promoter, followed by addition of the vector to an in vitro translation system such as a rabbit reticulocyte lysate or a wheat germ extract, containing an RNA polymerase corresponding to the promoter. RNA polymerase promoters are exemplified by T7, T3, SP6, and the like. The vectors containing these RNA polymerase promoters are exemplified by pKA1, pCDM8, pT3/T7 18, pT7/3 19, pBluescript II, and so on. Furthermore, the protein of the present invention can be expressed as the secreted form or the form incorporated into the microsome membrane, when a canine pancreas microsome or the like is added to the reaction system.

In the case where one of the protein of the present invention is produced by expressing the DNA in a microorganism such as *Escherichia coli* etc., a recombinant expression vector bearing the translated region of the cDNA of the present invention is constructed in an expression vector having an origin which can be replicated in the microorganism, a promoter, a ribosome-binding site, a cDNA-cloning site, a terminator etc. and, after transformation of the host cells with this expression vector, the resulting transformant is incubated, whereby the protein encoded by said cDNA can be produced on a large scale in the

microorganism. In this case, a protein fragment containing any region can be obtained by carrying out the expression with inserting an initiation codon and a termination codon in front of and behind the selected translated region. Alternatively, a fusion protein with another protein can be expressed. Only the portion of the protein encoded by this cDNA can be obtained by cleavage of this fusion protein with a suitable protease. The expression vector for *Escherichia coli* is exemplified by the pUC series, pBluescript II, the pET expression system, the pGEX expression system, and so on.

In the case where one of the proteins of the present invention is produced by expressing the DNA in eucaryotic cells, the protein of the present invention can be produced as a secretory protein or as a membrane protein on the cell-membrane surface, when the translated region of this cDNA is introduced into an expression vector for eucaryotic cells that has a promoter, a splicing region, a poly(A) addition site, etc., followed by introduction into the eucaryotic cells. The expression vector is exemplified by pKA1, pED6dpc2, pCDM8, pSVK3, pMSG, pSVL, pBK-CMV, pBK-RSV, EBV vector, pRS, pYES2, and so on. Examples of eucaryotic cells to be used in general include mammalian cultured cells such as simian kidney cells COS7, Chinese hamster ovary cells CHO, etc., budding yeasts, fission yeasts, silkworm cells, Xenopus oocytes, and so on, but any eucaryotic cells may be used, provided that they are capable of expressing the proteins of the present invention. The expression vector can be introduced into the eucaryotic cells by methods known in the art such as the electroporation method, the calcium phosphate method, the liposome method, the DEAE-dextran method, and so on.

After one of the proteins of the present invention is

expressed in prokaryotic cells or eucaryotic cells, the objective protein can be isolated from the culture and purified by a combination of separation procedures known in the art. Such examples include treatment with a denaturing agent such as urea or a detergent, sonication, enzymatic digestion, salting-out or solvent precipitation, dialysis, centrifugation, ultrafiltration, gel filtration, SDS-PAGE, isoelectric focusing, ion-exchange chromatography, hydrophobic chromatography, affinity chromatography, reverse phase chromatography, and so on.

The proteins of the present invention include peptide fragments (5 amino acid residues or more) containing any partial amino acid sequence in the amino acid sequences represented by SEQ ID Nos. 1. to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130. These peptide fragments can be utilized as antigens for preparation of antibodies. Hereupon, among the proteins of the present invention, those having the signal sequences are secreted in the form of mature proteins, after the signal sequences are removed. Therefore, these mature proteins shall come within the scope of the present invention. The N-terminal amino acid sequences of the mature proteins can be easily determined by using the method for the determination of cleavage site of a signal sequence [JP 8-187100 A]. Furthermore, some membrane proteins undergo the processing on the cell surface to be converted to the secretory forms. Such proteins or peptides in the secretory forms shall come within the scope of the present invention. In the case where sugar chain-binding sites are present in the amino acid sequences, expression in appropriate eucaryotic cells affords proteins to which sugar chains are attached. Accordingly, such proteins or peptides to which sugar chains are attached shall come within the

scope of the present invention.

The DNAs of the present invention include all the DNAs coding for the above-mentioned proteins. These DNAs can be obtained by using a method by chemical synthesis, a method by cDNA cloning, and so on.

The cDNAs of the present invention can be cloned, for example, from cDNA libraries derived from the human cells. These cDNAs are synthesized by using as templates poly(A)$^+$ RNAs extracted from human cells. The human cells may be cells delivered from the human body, for example, by the operation or may be the cultured cells. The cDNAs can be synthesized by using any method selected from the Okayama-Berg method [Okayama, H. and Berg, P., Mol. Cell. Biol. 2: 161-170 (1982)], the Gubler-Hoffman method [Gubler, U. and Hoffman, J. Gene 25: 263-269 (1983)], and so on, but it is preferred to use the capping method [Kato, S. et al., Gene 150: 243-250 (1994)], as exemplified in Examples, in order to obtain a full-length clone in an effective manner. In addition, commercially available, human cDNA libraries can be utilized. Cloning of the cDNAs of the present invention from the cDNA libraries can be carried out by synthesis of an oligonucleotide on the basis of base sequences of any portion in the cDNA of the present invention, followed by screening using this oligonucleotide as the probe according to the colony or plaque hybridization by a method known in the art. In addition, the cDNA fragments of the present invention can be prepared by synthesis of oligonucleotides which hybridize with both termini of the objective cDNA fragment, followed by the usage of these oligonucleotides as the primers for the RT-PCR method using an mRNA isolated from human cells.

The cDNAs of the present invention are characterized by

comprising either of the base sequences represented by SEQ ID Nos. 11 to 20, 41 to 50, 71 to 80, 101 to 110, and 131 to 140 or the base sequences represented by SEQ ID Nos. 21 to 30, 51 to 60, 81 to 90, 111 to 120, and 141 to 150. Table 1 summarizes the clone number (HP number), the cells from which the cDNA was obtained, the total base number of the cDNA, and the number of the amino acid residues of the encoded protein, for each of the cDNAs.

Table 1

SEQ ID No.	HP number	Cells	Base number	Number of amino acid residues
1, 11, 21	HP01550	Stomach cancer	510	125
2, 12, 22	HP02593	Saos-2	697	131
3, 13, 23	HP10195	HT-1080	1619	242
4, 14, 24	HP10423	U-2 OS	1066	264
5, 15, 25	HP10506	Stomach cancer	618	112
6, 16, 26	HP10507	Stomach cancer	1021	146
7, 17, 27	HP10548	Stomach cancer	1432	344
8, 18, 28	HP10566	Stomach cancer	601	97
9, 19, 29	HP10567	Stomach cancer	585	124
10, 20, 30	HP10568	Stomach cancer	1100	327
31, 41, 51	HP01426	Stomach cancer	1065	313
32, 42, 52	HP02515	Saos-2	937	229
33, 43, 53	HP02575	Saos-2	1678	467
34, 44, 54	HP10357	Stomach cancer	467	99
35, 45, 55	HP10447	Liver	875	189
36, 46, 56	HP10477	Liver	1256	363
37, 47, 57	HP10513	Stomach cancer	884	249
38, 48, 58	HP10540	Saos-2	589	98
39, 49, 59	HP10557	Stomach cancer	673	172
40, 50, 60	HP10563	Saos-2	1425	120
61, 71, 81	HP01467	HT-1080	1436	307
62, 72, 82	HP01956	Liver	997	183
63, 73, 83	HP02545	Saos-2	1753	327
64, 74, 84	HP02551	Saos-2	1117	223
65, 75, 85	HP02631	Saos-2	1380	48
66, 76, 86	HP02632	HT-1080	1503	371
67, 77, 87	HP10488	Liver	733	90
68, 78, 88	HP10538	Saos-2	3768	499
69, 79, 89	HP10542	Stomach cancer	770	106
70, 80, 90	HP10571	Stomach cancer	1229	152

91, 101, 111	HP01470	Stomach cancer	1619	358
92, 102, 112	HP02419	Stomach cancer	2054	226
93, 103, 113	HP02631	Saos-2	1380	195
94, 104, 114	HP02695	Stomach cancer	1292	339
95, 105, 115	HP10031	Saos-2	2168	487
96, 106, 116	HP10530	Saos-2	1357	393
97, 107, 117	HP10541	Stomach cancer	711	196
98, 108, 118	HP10550	Stomach cancer	651	107
99, 109, 119	HP10590	HT-1080	1310	350
100, 110, 120	HP10591	HT-1080	1400	107
121, 131, 141	HP01462	HT-1080	2050	483
122, 132, 142	HP02485	Stomach cancer	2746	334
123, 133, 143	HP02798	HT-1080	1136	267
124, 134, 144	HP10041	Saos-2	619	106
125, 135, 145	HP10246	KB	864	224
126, 136, 146	HP10392	U-2 OS	1527	258
127, 137, 147	HP10489	Stomach cancer	659	110
128, 138, 148	HP10519	Stomach cancer	710	91
129, 139, 149	HP10531	Saos-2	2182	344
130, 140, 150	HP10574	Stomach cancer	2773	428

Hereupon, the same clones as the cDNAs of the present invention can be easily obtained by screening of the cDNA libraries constructed from the human cell lines or human tissues utilized in the present invention by the use of an oligonucleotide probe synthesized on the basis of the cDNA base sequence described in any of SEQ ID Nos. 11 to 30, 41 to 60, 71 to 90, 101 to 120, and 131 to 150.

In general, the polymorphism due to the individual difference is frequently observed in human genes. Accordingly, any cDNA in which one or plural nucleotides are inserted, deleted and/or substituted with other nucleotides in SEQ ID Nos. 11 to 30, 41 to 60, 71 to 90, 101 to 120, and

131 to 150 shall come within the scope of the present invention.

In a similar manner, any protein in which one or plural amino acids are inserted, deleted and/or substituted with other amino acids shall come within the scope of the present invention, as far as the protein possesses the activity of any protein having the amino acid sequences represented by SEQ ID Nos. 1 to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130.

The cDNAs of the present invention include cDNA fragments (10 bp or more) containing any partial base sequence in the base sequences represented by SEQ ID Nos. 11 to 20, 41 to 50, 71 to 80, 101 to 110, and 131 to 140 or in the base sequences represented by SEQ ID Nos. 21 to 30, 51 to 60, 81 to 90, 111 to 120, and 141 to 150. Also, DNA fragments consisting of a sense strand and an anti-sense strand shall come within this scope. These DNA fragments can be utilized as the probes for the genetic diagnosis.

In addition to the activities and uses described above, the polynucleotides and proteins of the present invention may exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

Research Uses and Utilities

The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant

protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodiesusing DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine

levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be

administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular

Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol. 149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ, Schreiber, R.D. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6- Nordan, R. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark,S.C. and Turner, K.J. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp.

6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

<u>Immune Stimulating or Suppressing Activity</u>

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial orfungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp.

and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent

has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or

tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function in vivo on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating

autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the commoncold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the

transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and , microglobulin protein or an MHC class

II chain protein and an MHC class II chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowmanet al., J.

Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In vitro antibody production, Mond, J.J. and Brunswick, M. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965,

1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

<u>Hematopoiesis Regulating Activity</u>

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to

stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and

Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

<u>Tissue Growth Activity</u>

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is

not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and

in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head

trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon);

International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

<u>Activin/Inhibin Activity</u>

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among

other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among

other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis)consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result,such a protein is expected to be useful in treatment of various coagulation disorders (includinghereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include,

without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in:Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W.Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22),

Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of ytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A

protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or caricadic cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of

embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

Examples

The present invention is specifically illustrated in more detail by the following Examples, but Examples are not intended to restrict the present invention. The basic operations with regard to the recombinant DNA and the enzymatic reactions were carried out according to the literature ["Molecular Cloning. A Laboratory Manual", Cold Spring Harbor Laboratory, 1989]. Unless otherwise stated, restrictive enzymes and a variety of modification enzymes to be used were those available from Takara Shuzo. The buffer compositions and the reaction conditions for each of the enzyme reactions were as described in the manufacturer's instructions. The cDNA synthesis was carried out according to the literature [Kato, S. et al., Gene 150: 243-250 (1994)].

(1) Selection of cDNAs Encoding Proteins Having Hydrophobic Domains

The cDNA library of fibrosarcoma cell line HT-1080 (WO98/11217), the cDNA library of osteosarcoma cell line Saos-2 (WO97/33993), the cDNA library of osteosarcoma cell line U-2 OS (WO98/21328), the cDNA library of epidermoid

carcinoma cell line KB (WO98/11217), the cDNA library of tissues of stomach cancer delivered by the operation (WO98/21328), the cDNA library of liver tissue delivered by the operation (WO98/21328), and were used for the cDNA libraries. Full-length cDNA clones were selected from respective libraries and the whole base sequences thereof were determined to construct a homo-protein cDNA bank consisting of the full-length cDNA clones. The hydrophobicity/hydrophilicity profiles were determined for the proteins encoded by the full-length cDNA clones registered in the homo-protein cDNA bank by the Kyte-Doolittle method [Kyte, J. & Doolittle, R. F., J. Mol. Biol. 157: 105-132 (1982)] to examine the presence or absence of a hydrophobic region. Any clone that has a hydrophobic region being putative as a secretory signal or a transmembrane domain in the amino acid sequence of the encoded protein was selected as a clone candidate.

(2) Protein Synthesis by In Vitro Translation

The plasmid vector bearing the cDNA of the present invention was used for in vitro transcription/translation with a T_NT rabbit reticulocyte lysate kit (Promega). In this case, [^{35}S]methionine was added to label the expression product with a radioisotope. Each of the reactions was carried out according to the protocols attached to the kit. Two micrograms of the plasmid was subjected to the reaction at 30°C for 90 minutes in the reaction solution of a total volume of 25 μl containing 12.5 μl μ of T_NT rabbit reticulocyte lysate, 0.5 μl of a buffer solution (attached to the kit), 2 μl of an amino acid mixture (without methionine), 2 μl of [^{35}S]methionine (Amersham) (0.37 MBq/μl), 0.5 μl of T7 RNA polymerase, and 20 U of RNasin. Also, an experiment in the presence of a membrane system was carried

out by adding to this reaction system 2.5 μl of a canine pancreas microsome fraction (Promega). To 3 μl of the resulting reaction solution was added 2 μl of the SDS sampling buffer (125 mM Tris-hydrochloric acid buffer, pH 6.8, 120 mM 2-mercaptoethanol, 2% SDS solution, 0.025% bromophenol blue, and 20% glycerol) and the resulting mixture was heated at 95°C for 3 minutes and then subjected to SDS-polyacrylamide gel electrophoresis. The molecular weight of the translation product was determined by carrying out the autoradiography.

(3) Expression by COS7

Escherichia coli cells bearing the expression vector for the protein of the present invention was incubated at 37°C for 2 hours in 2 ml of the 2xYT culture medium containing 100 μg/ml of ampicillin, the helper phage M13KO7 (50 μl) was added, and the incubation was continued at 37°C overnight. A supernatant separated by centrifugation underwent precipitation with polyethylene glycol to obtain single-stranded phage particles. These particles were suspended in 100 μl of 1 mM Tris-0.1 mM EDTA, pH 8 (TE).

The cultured cells derived from simian kidney, COS7, were incubated at 37°C in the presence of 5% CO_2 in the Dulbecco's modified Eagle's culture medium (DMEM) containing 10% fetal calf serum. Into a 6-well plate (Nunc, well diameter: 3 cm) were inoculated with 1 x 10^5 COS7 cells and incubation was carried out at 37°C for 22 hours in the presence of 5% CO_2. After the culture medium was removed, the cell surface was washed with a phosphate buffer solution and then washed again with DMEM containing 50 mM Tris-hydrochloric acid (pH 7.5) (TDMEM). To the resulting cells was added a suspension of 1 μl of the single-stranded phage suspension, 0.6 ml of the DMEM culture medium, and 3 μl of

TRANSFECTAM™ (IBF) and the resulting mixture was incubated at 37°C for 3 hours in the presence of 5% CO_2. After the sample solution was removed, the cell surface was washed with TDMEM, 2 ml per well of DMEM containing 10% fetal calf serum was added, and the incubation was carried out at 37°C for 2 days in the presence of 5% CO_2. After the culture medium was replaced by a culture medium containing [^{35}S]cystine or [^{35}S]methionine, the incubation was carried out for one hour. After the culture medium and the cells were separated by centrifugation, proteins in the culture medium fraction and the cell-membrane fraction were subjected to SDS-PAGE.

(4) Clone Examples

<HP01550> (SEQ ID Nos. 1, 11, and 21)

Determination of the whole base sequence of the cDNA insert of clone HP01550 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 65-bp 5'-untranslated region, a 378-bp ORF, and a 67-bp 3'-untranslated region. The ORF codes for a protein consisting of 125 amino acid residues and there existed one putative transmembrane domain. Figure 1 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 15 kDa that was almost identical with the molecular weight of 13,825 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Caenorhabditis elegans hypothetical protein F45G2.c (GenBank Accession No. Z93382). Table 2 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the C.

elegans hypothetical protein F45G2.c (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 44.5% in the entire region.

Table 2

```
HP  MAKYLAQIIVMGVQVVGRAFARALRQEF------AASRAAADARGRAGHRSAAASNLS-
          .. . . ..*..*..**.*.*.      **..**..... .. *..*.** .
CE MPWRTALKVALAAGEAVAKALTRAVRDEIKQTQQAAARHAASTGQSASETRENANSNAKL
HP GLSLQEAQQILNV-SKLSPEEVQKNYEHLFKVNDKSVGGSFYLQSKVVRAKERLDEEL-K
   *.**.*. ***** . *..***.*.*****..**** **..****** *****.***. .
CE GISLEESLQILNVKTPLNREEVEKHYEHLFNINDKSKGGTLYLQSKVFRAKERIDEEFGR
HP IQAQEDREKGQMPHT
   *. .*...*.. ..*
CE IELKEEKKKEENAKTE
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA338859) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP02593> (SEQ ID Nos. 2, 12, and 22)

Determination of the whole base sequence of the cDNA insert of clone HP02593 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 103-bp 5'-untranslated region, a 396-bp ORF,

and a 198-bp 3′-untranslated region. The ORF codes for a protein consisting of 131 amino acid residues and there existed four putative transmembrane domains at the C-terminus. Figure 2 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of a high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to a human OB-R gene-related protein (EMBL Accession No. Y12670). Table 3 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human OB-R gene-related protein (OB). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 67.9% in the entire region.

Table 3

```
HP MAGIKALISLSFGGAIGLMFLMLGCALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTD
   ***.***..***.***** ********  *. *******.*. .****: **.*.. *.*
OB MAGVKALVALSFSGAIGLTFLMLGCALEDYGVYWPLFVLIFHAISPIPHFIAKRVTYDSD
HP AMSNACKELAIFLTTGIVVSAFGLPIVFARAHLIEWGACALVLTGNTVIFATILGFFLVF
   * *.**.*** *.**********.*...**. .*.****.***.**.*** ** ****.*
OB ATSSACRELAYFFTTGIVVSAFGFPVILARVAVIKWGACGLVLAGNAVIFLTIQGFFLIF
HP GSNDDFSWQQW
   *..*****.**
OB GRGDDFSWEQW
```


Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA306490) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10195> (SEQ ID Nos. 3, 13, and 23)

Determination of the whole base sequence of the cDNA insert of clone HP10195 obtained from cDNA library of human fibrosarcoma HT-1080 revealed the structure consisting of a 286-bp 5′-untranslated region, a 729-bp ORF, and a 604-bp 3′-untranslated region. The ORF codes for a protein consisting of 242 amino acid residues and there existed one putative transmembrane domain at the C-terminus. Figure 3 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 32 kDa that was somewhat larger than the molecular weight of 27,300 predicted from the ORF. When expressed in COS7 cells, an expression product of about 21 kDa was observed in the supernatant fraction and the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein has revealed the registration of sequences that were similar to the Aplysia VAP-33 (SWISS-PROT Accession No. P53173). Table 4 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the Aplysia VAP-33 (AP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the

present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 46.5% in the entire region.

Table 4

```
HP MAKHEQILVLDPPTDLKFKGPFTDVVTTNLKLRNPSDRKVCFKVKTTAPRRYCVRPNSGI
   **.*** *.*.*...*.**********..***.**.**..*********.**********
AP MASHEQALILEPAGELRFKGPFTDVVTADLKLSNPTDRRICFKVKTTAPKRYCVRPNSGI
HP IDPGSTVTVSVMLQPFDYDPNEKSKHKFMVQTIFAPPNTSD-MEAVWKEAKPDELMDSKL
   ..* ....*.******.******.*******...** .. .  * .**.* *..***.**
AP LEPKTSIAVAVMLQPFNYDPNEKNKHKFMVQSMYAPDHVVESQELLWKDAPPESLMDTKL
HP RCVFEMPNENDKLNDMEPSK--------------AVPLNASKQDGPMPKP-HSVSLNDTE
   *******.....  ....*.              . .....* ... **.  .*. ....
AP RCVFEMPDGSHQAPASDASRATDAGAHFSESALEDPTVASRKTETQSPKRVGAVGSAGED
HP TRKLMEECKRLQGEMMKLSEENRHLRDEGLRLRKVAHSD--KPGSTSTASFRDNVTSPLP
   ..** .* *. *.*. .*..**..*.***.****** .*  .*.. .... ........*
AP VKKLQHELKKAQSEITSLKGENSQLKDEGIRLRKVAMTDTVSPTPLNPSPAPAAAVRAFP
HP SLLVVIAAIFIGFFLGKFIL
   ... *.***..*...***.*
AP PVVYVVAAIILGLIIGKFLL
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA447905) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10423> (SEQ ID Nos. 4, 14, and 24)

Determination of the whole base sequence of the cDNA insert of clone HP10423 obtained from cDNA library of human osteosarcoma cell line U-2 OS revealed the structure consisting of a 64-bp 5'-untranslated region, a 795-bp ORF, and a 207-bp 3'-untranslated region. The ORF codes for a protein consisting of 264 amino acid residues and there existed a secretory signal at the N-terminus and one putative transmembrane domain at the N-terminus. Figure 4 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 30 kDa that was almost identical with the molecular weight of 29,377 predicted from the ORF. When expressed in COS7 cells, an expression product of about 31 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. D80116) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10506> (SEQ ID Nos. 5, 15, and 25)

Determination of the whole base sequence of the cDNA insert of clone HP10506 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 53-bp 5'-untranslated region, a 339-bp ORF, and a 226-bp 3'-untranslated region. The ORF codes for a protein consisting of 112 amino acid residues and there existed one putative transmembrane domain. Figure 5 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-

Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 12 kDa that was almost identical with the molecular weight of 11,821 predicted from the ORF. When expressed in COS7 cells, an expression product of about 13 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA282544) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10507> (SEQ ID Nos. 6, 16, and 26)

Determination of the whole base sequence of the cDNA insert of clone HP10507 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 412-bp 5'-untranslated region, a 441-bp ORF, and a 168-bp 3'-untranslated region. The ORF codes for a protein consisting of 146 amino acid residues and there existed a secretory signal at the N-terminus and one putative transmembrane domain at the C-terminus. Figure 6 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 19 kDa that was somewhat larger than the molecular weight of 16,347 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA424759) in ESTs, but, since they

are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10548> (SEQ ID Nos. 7, 17, and 27)

Determination of the whole base sequence of the cDNA insert of clone HP10548 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 330-bp 5'-untranslated region, a 1035-bp ORF, and a 67-bp 3'-untranslated region. The ORF codes for a protein consisting of 344 amino acid residues and there existed four putative transmembrane domains. Figure 7 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of a high molecular weight.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA143152) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10566> (SEQ ID Nos. 8, 18, and 28)

Determination of the whole base sequence of the cDNA insert of clone HP10566 obtained from cDNA library of the human stomach cancer revealed the structure consisting of a 61-bp 5'-untranslated region, a 294-bp ORF, and a 246-bp 3'-untranslated region. The ORF codes for a protein consisting of 97 amino acid residues and there existed one putative transmembrane domain at the C-terminus. Figure 8 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 12 kDa that was almost identical with the molecular weight of 11,452 predicted from the ORF. When expressed in COS7 cells, an expression product of about 12 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. W79821) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10567> (SEQ ID Nos. 9, 19, and 29)

Determination of the whole base sequence of the cDNA insert of clone HP10567 obtained from cDNA library of the human stomach cancer revealed the structure consisting of a 77-bp 5'-untranslated region, a 375-bp ORF, and a 133-bp 3'-untranslated region. The ORF codes for a protein consisting of 124 amino acid residues and there existed one putative transmembrane domain at the C-terminus. Figure 9 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 14 kDa that was almost identical with the molecular weight of 14,484 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA428475) in ESTs, but, since they

are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10568> (SEQ ID Nos. 10, 20, and 30)

Determination of the whole base sequence of the cDNA insert of clone HP10568 obtained from cDNA library of the human stomach cancer revealed the structure consisting of a 56-bp 5'-untranslated region, a 984-bp ORF, and a 60-bp 3'-untranslated region. The ORF codes for a protein consisting of 327 amino acid residues and there existed a secretory signal at the N-terminus and one putative transmembrane domain at the C-terminus. Figure 10 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 36.5 kDa that was almost identical with the molecular weight of 34,326 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 40 kDa which is considered to have a sugar chain being attached. In addition, there exist in the amino acid sequence of this protein two sites at which N-glycosylation may occur (Asn-Leu-Thr at position 138 and Asn-Leu-Ser at position 206). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from valine at position 24. When expressed in COS7 cells, an expression product of about 31 kDa was observed in the supernatant fraction and the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein has revealed that the protein was similar to the human cell-surface A33 antigen

(SWISS-PROT Accession No. Q99795). Table 5 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human cell-surface A33 antigen (A3). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 30.0% in the N-terminal region of 243 residues.

Table 5

```
HP MAELPGPFLCGALLGFLCLSGLAVEVKVPTEPLSTPLGKTAELTCTYSTSVGDSFAL-EW
                               *..*..* . *... **...*.*** **.... .* .*
A3   MVGKMWPVLWTLCAVRVTVDAISVETPQDVLRASQGKSVTLPCTYHTSTSSREGLIQW
HP SFVQPGKPISESHPILYFTNGHLYPTGSKSKRVSLLQNPPTVGVATLKLTDVHPSDTGTY
   . .    . .*.  *  *.* . *  *.  *.   . * .. . *.......  .*.***
A3 DKLL--LTHTERVVIWPFSNKN-YIHGELYKNRVSISNNAEQSDASITIDQLTMADNGTY
HP LCQVNNPPDFYTNGLGLINLTVLVPPSNPLCSQSGQTSVGGSTALRCSSSEGAPKPVYNW
    * *.  .*. .*. . ..* ******.* *. .*.* .*....* * *.**.*.* *.*
A3 ECSVSLMSDLEGNTKSRVRLLVLVPPSKPECGIEGETIIGNNIQLTCQSKEGSPTPQYSW
HP VRLGTFPTPSPGSMVQDEVSGQLILTNLSLTSSGTYRCVATNQMGSASCELTLSVTEPS-
    * ...    *  ..* . . .. *.*.* ..** * *...*. *.. *..*..* .**
A3 KRYNILNQEQP--LAQPASGQPVSLKNISTDTSGYYICTSSNEEGTQFCNITVAVRSPSM
HP -QGRVAGALIGVLLGVLLLSVAAFCLVRFQKERGKKPKETYGGSDLREDAIAPGISEHTC
  .   .*  .**. ....... .*
A3 NVALYVGIAVGVVAALIIIGIIIYCCCCRGKDDNTEDKEDARPNREAYEEPPEQLRELSR
HP MRADSSKGFLERPSSASTVTTTKSKLPMVV

A3 EREEEDDYRQEEQRSTGRESPDHLDQ
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration

of sequences that shared a homology of 90% or more (for example, Accession No. T24595) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP01426> (SEQ ID Nos. 31, 41, and 51)

Determination of the whole base sequence of the cDNA insert of clone HP01426 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 1-bp 5'-untranslated region, a 942-bp ORF, and a 122-bp 3'-untranslated region. The ORF codes for a protein consisting of 313 amino acid residues and there existed a putative secretory signal. Figure 11 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 36 kDa that was almost identical with the molecular weight of 34,955 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 38 kDa which is considered to have a sugar chain being attached after secretion. In addition, there exists in the amino acid sequence of this protein one site at which N-glycosylation may occur (Asn-Ser-Ser at position 163). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from tryptophan at position 17. When expressed in COS7 cells, an expression product of about 39 kDa was observed in the supernatant fraction and the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the

protein was similar to the Xenopus laevis cortical granule lectin (EMBL Accession No. X82626). Table 6 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the X. laevis cortical granule lectin (XL). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 67.9% in the region other than the N-terminal region.

Table 6

```
HP MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT
   *     **                   *           ********. .* **.* * .
XL MLVHILLLLVTGGLSQSCEPVVIVASKNMVKQLDCDKFRSCKEIKDSNEEAQDGIYTLTS
HP ENGVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANY
   ..*. *********..*************.* ****.*********..************
XL SDGISYQTFCDMTTNGGGWTLVASVHENNMAGKCTIGDRWSSQQGNRADYPEGDGNWANY
HP NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLG
   ******..**************.* .**.******.*.  ****** ****..*.* . *
XL NTFGSAGGATSDDYKNPGYYDIEAYNLGVWHVPNKTPLSVWRNSSLQRYRTTDGILFKHG
HP HNLFGIYQKYPVKYGEGKCWTDNGPVIPVVYDFGDAQKTASYYSPYGQREFTAGFVQFRV
    ***..*. ****** *.* .*.**..*****.*.*. ***.***  ...**.*..***
XL GNLFSLYRIYPVKYGIGSCSKDSGPTVPVVYDLGSAKLTASFYSPDFRSQFTPGYIQFRP
HP FNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSSS
   .*.*.** ***.**....**.** ***********.*.*****...*..****.   *..
XL INTEKAALALCPGMKMESCNVEHVCIGGGGYFPEADPRQCGDFAAYDFNGYGTKKFNSAG
HP REITEAAVLLFYR
   ***********
XL IEITEAAVLLFYL
```


Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R06009) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP02515> (SEQ ID Nos. 32, 42, and 52)

Determination of the whole base sequence of the cDNA insert of clone HP02515 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 176-bp 5'-untranslated region, a 690-bp ORF, and a 71-bp 3'-untranslated region. The ORF codes for a protein consisting of 229 amino acid residues and there existed a putative secretory signal at N-terminus and one putative transmembrane domain at the C-terminus. Figure 12 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 27 kDa that was almost identical with the molecular weight of 26,000 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 25.5 kDa from which the secretory signal is considered to have been cleaved. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from phenylalanine at position 28.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human T1/ST2 receptor binding protein (GenBank Accession No. U41804). Table 7 shows the

comparison between amino acid sequences of the human protein of the present invention (HP) and the human T1/ST2 receptor binding protein (T1). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 55.8% in the entire region.

Table 7

```
HP   MGDKIWLPFFPVLLLAALPPVLLPGAAGFTPSLDSDFTFTLPAGQKECFYQPMPLKASLE
          *.... **  .*** ..*.** .*  *..*** ****.*.****. * .****
T1  MMAAGAALALALWLL--MPPVEV-GGAGPPPIQDGEFTFLLPAGRKQCFYQSAPANASLE
HP  IEYQVLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVE-TEVGDYMFCFDNTFSTISEK
    .****..*****.** *.**.*   ** * **.******* **.***..****.*******
T1  TEYQVIGGAGLDVDFTLESPQGVLLVSESRKADGVHTVEPTEAGDYKLCFDNSFSTISEK
HP  VIFFELILDNMGEQAQEQEDWKKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLR
    ..*****.*.. ....* *.* . .. ...**.*.*** ***.....**..* .. .***
T1  LVFFELIFDSL-QDDEEVEGWAEAVEPEEMLDVKMEDIKESIETMRTRLERSIQMLTLLR
HP  AFEARDRNIQESNFDRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSRT
    ********.**.*..****** **..*...*...**. **..*.***  .*
T1  AFEARDRNLQEGNLERVNFWSAVNVAVLLLVAVLQVCTLKRFFQDKRPVPT
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA381943) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP02575> (SEQ ID Nos. 33, 43, and 53)

Determination of the whole base sequence of the cDNA insert of clone HP02575 obtained from cDNA library of human osteosarcome cell line Saos-2 revealed the structure consisting of a 55-bp 5'-untranslated region, a 1404-bp ORF, and a 219-bp 3'-untranslated region. The ORF codes for a protein consisting of 467 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 13 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 52 kDa that was almost identical with the molecular weight of 54,065 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 57 kDa which is considered to have a sugar chain being attached afetr secretion. In addition, there exist in the amino acid sequence of this protein three sites at which N-glycosylation may occur (Asn-Arg-Thr at position 171, Asn-Ser-Thr at position 239 and Asn-Asp-Thr at position 377). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from histidine at position 29. When expressed in COS7 cells, an expression product of about 55 kDa was observed in the supernatant fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human α-L-fucosidase (SWISS-PROT Accession No. P04066). Table 8 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human α-L-fucosidase (FC). Therein,

the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 54.8% in the entire region.

Table 8

```
HP MRPQELPRLAFPLLLLLLLLLPPPPC-PAHSATRFDPTWESLDARQLPAWFDQAKFGIFI
                .******.* .. .  .*... *..*.* ***.*.******.****.**
FC    MRSRPAGPALLLLLLFLGAAESVRRAQPPRRYTPDWPSLDSRPLPAWFDEAKFGVFI
HP HWGVFSVPSFGSEWFWWYWQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWAD
   ********..*******.** *  *.*  **.*****.*.*.**** ***.**....***
FC HWGVFSVPAWGSEWFWWHWQGEGRPQYQRFMRDNYPPGFSYADFGPQFTARFFHPEEWAD
HP IFQASGAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGL
   .***.****.***.******* * *  *****, * **.**.* **...*.*.* ..*.**
FC LFQAAGAKYVVLTTKHHEGFTNWPSPVSWNWNSKDVGPHRDLVGELGTALRKR-NIRYGL
HP YYSLFEWFHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWN
   *.**.******.* *....*....*  .**.****.***.*.*...****. . ** ***
FC YHSLLEWFHPLYLLDKKNGFKTQHFVSAKTMPELYDLVNSYKPDLIWSDGEWECPDTYWN
HP STGFLAWLYNESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDK
   **.**.****.***...**.*****... *.***.*.*.*...*  *  **** * .***
FC STNFLSWLYNDSPVKDEVVVNDRWGQNCSCHHGGYYNCEDKFKPQSLPDHKWEMCTSIDK
HP LSWGYRREAGISDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQMGSW
   .******. ..**  . .*....**.*** *** *.***** ** *  .*.*** ..*.*
FC FSWGYRRDMALSDVTEESEIISELVQTVSLGGNYLLNIGPTKDGLIVPIFQERLLAVGKW
HP LKVNGEAIYETHTWRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGA
   *..******.....** * .. *..******  ..  ******.**..* * *. * .. ..
FC LSINGEAIYASKPWRVQWEKNTTSVWYTSKGSA--VYAIFLHWPENGVLNLESPITT-ST
HP TEVKLLGHGQPLNWISLEQNGIMVELPQLTIHQMPCKWGWALALTNVI
   *....**    *.* .  ..*....****.  ..* ...*.. **.*
FC TKITMLGIQGDLKWSTDPDKGLFISLPQLPPSAVPAEFAWTIKLTGVK
```


Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. N28668) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10357> (SEQ ID Nos. 34, 44, and 54)

Determination of the whole base sequence of the cDNA insert of clone HP10357 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 113-bp 5'-untranslated region, a 300-bp ORF, and a 54-bp 3'-untranslated region. The ORF codes for a protein consisting of 99 amino acid residues and there existed two putative transmembrare domains. Figure 14 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 11 kDa that was almost identical with the molecular weight of 10,923 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA477156) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10447> (SEQ ID Nos. 35, 45, and 55)

Determination of the whole base sequence of the cDNA

insert of clone HP10447 obtained from cDNA library of human liver revealed the structure consisting of a 271-bp 5'-untranslated region, a 570-bp ORF, and a 34-bp 3'-untranslated region. The ORF codes for a protein consisting of 189 amino acid residues and there existed five putative transmembrare domains. Figure 15 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA296976) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10477> (SEQ ID Nos. 36, 46, and 56)

Determination of the whole base sequence of the cDNA insert of clone HP10477 obtained from cDNA library of human liver revealed the structure consisting of a 149-bp 5'-untranslated region, a 1092-bp ORF, and a 15-bp 3'-untranslated region. The ORF codes for a protein consisting of 363 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 16 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 40 kDa that was almost identical with the molecular weight of 39,884 predicted from the ORF.

The search of the protein data base using the amino

acid sequence of the present protein revealed that the protein was similar to the human peptidoglycan recognition protein (GenBank Accession No. AF076483). Table 9 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human peptidoglycan recognition protein (PG). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 54.8% in the entire region.

Table 9

```
HP MVDSLLAVTLAGNLGLTFLRGSQTQSHPDLGTEGCWDQLSAPRTFTLLDPKASLLTKAFL
HP NGALDGVILGDYLSRTPEPRPSLSHLLSQYYGAGVARDPGFRSNFRRQNGAALTSASILA
HP QQVWGTLVLLQRLEPVHLQLQCMSQEQLAQVAANATKEFTEAFLGCPAIHPRCRWGAAPY
                                                *..* **  * * .
PG                 MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALA-
HP RGRPKLLQLPLGFLYVHHTYVPAPPCTDFTRCAANMRSMQRYHQDTQGWGDIGYSFVVGS
   .. .. * *** .. * **  ....*.. ..*... *..*.** .* ** *.**.*..*.
PG SECAQHLSLPLRYVVVSHT--AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGE
HP DGYVVYEGRGWHWVGAHTLGH-NSRGFGVAIVGNYTAALPTEAALRTVRDTLPSCAVRAGL
   ** *******...***.    *....*....*** . .** .*.*.... * .*.* .*
PG DGLVYEGRGWNFTGAHSGHLWNPMSIGISFMGNYMDRVPTPQAIRAAQGLL-ACGVAQGA
HP LRPDYALLGHRQLVRTDCPGDALFDLLRTWPHFTATVKPRPARSVSKRSRREPPPRTLPA
   **..*.* ***.. ** .**..*..*...***.
PG LRSNYVLKGHRDVQRTLSPGNQLYHLIQNWPHYRSP
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration

of sequences that shared a homology of 90% or more (for example, Accession No. AA424759) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10513> (SEQ ID Nos. 37, 47, and 57)

Determination of the whole base sequence of the cDNA insert of clone HP10513 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 134-bp 5'-untranslated region, a 750-bp ORF, and a 0-bp 3'-untranslated region. The ORF codes for a protein consisting of 249 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 17 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 29 kDa that was almost identical with the molecular weight of 27,373 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human hypothetical protein KIAA0512 (GenBank Accession No. AB011084). Table 10 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human hypothetical protein KIAA0512 (KI). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 31.6% in the C-terminal region of 196 amino acid residues.

Table 10

```
HP                    MGGPRGAGWVAAGLLLGAGACYCIYRLTRGRRRG

KI RGRGRRPVAMQKRPFPYEIDEILGVRDLRKVLALLQKSDDPFIQQVALLTLSNNANYSCN
HP DRELGIRSSKSAEDLTDGSYDDVLNAEQLQKLLYLLESTEDPVIIERALITLGNNAAFSV
                    * .....* . * *. *.. .. . .. ..   *

KI QETIRKLGGLPIIANMINKTDPHIKEKALMAMNNLSENYENQGRLQVYMNKVMDDIMASN
HP NQAIIRELGGIPIVANKINHSNQSIKEKALNALNNLSVNVENQIKIKVQVLKLLLNLSEN
    .. .. .*   ... .*... * .  ......  ...  ..  ****..**.* *..**

KI LNSAVQVVGLKFLTNMTITNDYQHLLVNSIANF--FRLLSQGGGKIKVEILKILSNFAEN
HP PAMTEGLLRAQVDSSFLSLYDSHVAKEILLRVLTLFQNIKNCLKIEGHLAVQPTFTEGSL
   *.* . **..** .** ***.*.*..***...****. * . *. *  .   ..*..***

KI PDMLKKLLSTQVPASFSSLYNSYVESEILINALTLFEIIYDNLRAE--VFNYREFNKGSL
HP FFL-LHGEECAQKIRALVDHHDAEVKEKVVTIIPKI
   *.*   .. *..*****..***  ** **.... *.

KI FYLCTTSGVCVKKIRALANHHDLLVKVKVIKLVNKF
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. N92228) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10540> (SEQ ID Nos. 38, 48, and 58)

Determination of the whole base sequence of the cDNA insert of clone HP10540 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure

consisting of a 47-bp 5'-untranslated region, a 297-bp ORF, and a 245-bp 3'-untranslated region. The ORF codes for a protein consisting of 98 amino acid residues and there existed two putative transmembrane domains. Figure 18 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Caenorhabditis elegans hypothetical protein CEF49C12.12 (GenBank Accession No. Z68227). Table 11 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the C. elegans hypothetical protein CEF49C12.12 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 36.1% in the entire region.

Table 11

```
HP M-ASLLCCGPKLAACGIVLSAWGVIMLIMLGIFFNVHSAVLIEDVPFTEKDFENGPQNIY
   *       *** *   * * **** *  ** **      *  *  * *        *
CE MGKICPLMGPKMSAFCMVMSVWGVIFLGLLGVFFYIQAVTLFPDLHF-EGHGKVPSSVID
HP NLYEQVSYNCFIAAGLYLLLGGFSFCQVRLNKRKEYMVR
     *      * ******        * *   **
CE AKYNEKATQCWIAAGLYAVTLIAVFWQ---NKYNTAQIF
```


Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA420715) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10557> (SEQ ID Nos. 39, 49, and 59)

Determination of the whole base sequence of the cDNA insert of clone HP10557 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 24-bp 5'-untranslated region, a 519-bp ORF, and a 130-bp 3'-untranslated region. The ORF codes for a protein consisting of 172 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 19 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 32 kDa that was larger than the molecular weight of 18,844 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 39 kDa which is considered to have been subjected to some modification after secretion. In addition, there exist in the amino acid sequence of this protein no site at which N-glycosylation may occur. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glycine at position 32. When expressed in COS7 cells, an expression product of about 20 kDa was observed in the supernatant fraction and the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human progesterone binding protein (EMBL Accession No. AJ002030). Table 12 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human progesterone binding protein (PG). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 30.5% in the C-terminal region of 151 amino acid residues.

Table 12

```
HP                                                       MVGPAP

PG MAAGDGDVKLGTLGSGSESSNDGGSESPGDAGAAAEGGGWAAAALALLTGGGEMLLNVAL
HP RRRLRPLAALALVLALAPGLPTARAGQTPRPAERGPPV--RLFTEEELARYGGEEEDQPI
                    **  .. .. . .**.. *..  * *. *.* .*.* . ...*
PG VALVLLGAYRLWVRWGRRGLGAGAGAGEESPATSLPRMKKRDFSLEQLRQYDG-SRNPRI
HP YLAVKGVVFDVTSGKEFYGRGAPYNALTGKDSTRGVAKMSLDPADLTHDTTGLTAKELEA
    ***.* *****.*..***...**. ..*.*..**.*...** ..* .. ..*.. .  .
PG LLAVNGKVFDVTKGSKFYGPAGPYGIFAGRDASRGLATFCLDKDALRDEYDDLSDLNAVQ
HP LDEV--FTKVYKAKYPIVGYTARRILNEDGSPNLDFKPEDQPHFDIKDEF
   ...*  ... .*.**   .*.. *.*. ...*. ... *.... . *..
PG MESVREWEMQFKEKY---DYVG-RLLKPGEEPS-EYTDEEDTKDHNKQD
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for

example, Accession No. AA101709) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10563> (SEQ ID Nos. 40, 50, and 60)

Determination of the whole base sequence of the cDNA insert of clone HP10563 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 126-bp 5'-untranslated region, a 363-bp ORF, and a 936-bp 3'-untranslated region. The ORF codes for a protein consisting of 120 amino acid residues and there existed two putative transmembrane domains. Figure 20 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 18.5 kDa that was larger than the molecular weight of 13,180 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Arabidopsis thaliana hypothetical protein F27F23.15 (GenBank Accession No. AC003058). Table 13 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the A. thaliana hypothetical protein F27F23.15 (AT). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 35.5% in the entire region.

Table 13

```
HP MMPSRTNLATGIPSSKVKYSRLSSTDDGYIDLQFKKTPPKIPYKAIALATVLFLIGAFLI
                           *..* .*.  . ... . * *.*.**. *...*.. *
AT              MAYVDHAFSISDEDLMIGTSY-TVSNRPPVKEISLAVGLLVFGTLGI
HP IIGSLLLSGYISKGGADRAVPVLIIGILVFLPGFYHLRIAYYASKGYRGYSYDDIPDFDD
   ..* ..  . .. *. ....  ...* *.*.****. ****** ***.*.*...**
AT VLGFFMAYNRVG-GDRGHGIFFIVLGCLLFIPGFYYTRIAYYAYKGYKGFSFSNIPSV
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA083574) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP01467> (SEQ ID Nos. 61, 71, and 81)

Determination of the whole base sequence of the cDNA insert of clone HP01467 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 65-bp 5'-untranslated region, a 924-bp ORF, and a 447-bp 3'-untranslated region. The ORF codes for a protein consisting of 307 amino acid residues and there existed three putative transmembrane domains. Figure 21 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino

acid sequence of the present protein revealed that the protein was similar to the rat Sec22 homologue (GenBank Accession No. U42209). Table 14 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the rat Sec22 homologue (RN). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 94.6% in the N-terminal region of 241 amino acid residues. The protein of the present invention was longer by 53 amino acids at the C-terminus than the rat Sec22 homologue.

Table 14

```
HP MSMILSASVIRVRDGLPLSASTDYEQSTGMQECRKYFKMLSRKLAQLPDRCTLKTGHYNI
   *********.*************.***.*.***************.*********..**
RN MSMILSASVVRVRDGLPLSASTDCEQSAGVQECRKYFKMLSRKLAQFPDRCTLKTGRHNI
HP NFISSLGVSYMMLCTENYPNVLAFSFLDELQKEFITTYNMMKTNTAVRPYCFIEFDNFIQ
   ************************************************************
RN NFISSLGVSYMMLCTENYPNVLAFSFLDELQKEFITTYNMMKTNTAVRPYCFIEFDNFIQ
HP RTKQRYNNPRSLSTKINLSDMQTEIKLRPPYQISMCELGSANGVTSAFSVDCKGAGKISS
   ********************** **********.*************************
RN RTKQRYNNPRSLSTKINLSDMQMEIKLRPPYQIPMCELGSANGVTSAFSVDCKGAGKISS
HP AHQRLEPATLSGIVGFILSLLCGALNLIRGFHAIESLLQSDGDDFNYIIAFFLGTAACLY
   **************.**************************.**.*.************
RN AHQRLEPATLSGIVAFILSLLCGALNLIRGFHAIESLLQSDGEDFSYMIAFFLGTAACLY
HP QCYLLVYYTGWRNVKSFLTFGLICLCNMYLYELRNLWQLFFHVTVGAFVTLQIWLRQAQG
   *
RN QMICLCLQGRKERT
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA421925) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP01956> (SEQ ID Nos. 62, 72, and 82)

Determination of the whole base sequence of the cDNA insert of clone HP01956 obtained from cDNA library of human liver revealed the structure consisting of a 86-bp 5'-untranslated region, a 552-bp ORF, and a 359-bp 3'-untranslated region. The ORF codes for a protein consisting of 183 amino acid residues and there existed one putative transmembrane domain. Figure 22 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 20.5 kDa that was almost identical with the molecular weight of 20,073 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the yeast hypothetical protein 21.5 kDa (SWISS-PROT Accession No. P53073). Table 15 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the yeast hypothetical protein 21.5 kDa (SC). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology

of 34.3% in the C-terminal region of 108 amino acid residues.

Table 15

```
HP      MTAQGGLVANRGRRFKWAIELSGPGGGSRGRSDRGSGQGDSLYPVGYLDKQVPDTS

SC MSEQEPYEWAKHLLDTKYIEKYNIQNSNTLPSPPGFEGNSSKGNVTRKQQDATSQTTSLA
HP VQETDRILVEKRCWDIALGPLKQIPMNLFIMYMAGNTISIFPTMMVCMMAWRPIQALMAI
         .*  .. *.*** * * ****.*.  **.*...  *.*.* . *.   **.*....
SC QKNQITVLQVQKAWQIALQPAKSIPMNIFMSYMSGTSLQIIPIMTALMLLSGPIKAIFST
HP SATFK--MLESSSQKFLQGLVYLIGNLMGLALAV-Y-KCQSMGLLPTHASDWLAFIEPPE
   ...**  . ....*. .*. ...   . *. . . * * .****.*.  .***.
SC RSAFKPVLGNKATQSQVQTAMFMYIVFQGVLMYIGYRKLNSMGLIPNAKGDWLPWERIAH
HP RMEFSGGGLLL

SC YNNGLQWFSD
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA159753) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP02545> (SEQ ID Nos. 63, 73, and 83)

Determination of the whole base sequence of the cDNA insert of clone HP02545 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 133-bp 5'-untranslated region, a 984-bp ORF, and a 636-bp 3'-untranslated region. The ORF codes for a

protein consisting of 327 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain at the C-terminus. Figure 23 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the rat embigin (EMBL Accession No. AJ009698). Table 16 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the rat embigin (RN). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 65.4% in the entire region.

Table 16

```
HP MRALPGLLEARARTPRLLLLQCLLAAARPSSADGSAPDSPFTSPPLREEIMAN--NFSLE
   **. .** .  *.. .**** .****.**..* *...**.*** *.***.**.  *.***
RN MRSHTGLRALVAPGCSLLLL-YLLAATRPDRAVGDPADSAFTSLPVREEMMAKYANLSLE
HP SHNISLTEHSSMPVEKNITLERPSNVNLTCQFTTSGDLNAVNVTWKKDGEQLE--NNYLV
   ..******..... *.*********...*.* **...*. ..*******.. **  ::. .
RN TYNISLTEQTRVS-EQNITLERPSHLELECTFTATEDVMSMNVTWKKDDALLETTDGFNT
HP SATGSTLYTQYRFTIINSKQMGSYSCFFREEKEQRGTFNFKVPELHGKNKPLISYVGDST
   .  *.***.*****..******.****. **   *****..**..********.******
RN TKMGDTLYSQYRFTVFNSKQMGKYSCFLGEE--LRGTFNIRVPKVHGKNKPLITYVGDST
HP VLTCKCQNCFPLNWTWYSSNGSVKVPVGVQM-NKYVINGTYANETKLKITQLLEEDGESY
   **.*.****.******* ***...**..*.. .*. ***.********...******.**
RN VLKCECQNCLPLNWTWYMSNGTAQVPIDVHVNDKFDINGSYANETKLKVKHLLEEDGGSY
HP WCRALFQLGESEEHIELVVLSYLVPLKPFLVIVAEVILLVATILLCEKYTQKKKHSDEG
   **** *.********.*****..*******.*.********.***** ******...*.*
RN WCRAAFPLGESEEHIKLVVLSFMVPLKPFLAIIAEVILLVAIILLCEVYTQKKKNDPDDG
HP KEFEQIEQLKSDDSNGIENNVPRHRKNESLGQ
   ***********************.**..* .*
RN KEFEQIEQLKSDDSNGIENNVPRYRKTDSGDQ
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA312629) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP02551> (SEQ ID Nos. 64, 74, and 84)

Determination of the whole base sequence of the cDNA insert of clone HP02551 obtained from cDNA library of human

osteosarcoma cell line Saos-2 revealed the structure consisting of a 61-bp 5'-untranslated region, a 672-bp ORF, and a 384-bp 3'-untranslated region. The ORF codes for a protein consisting of 223 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 24 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 27 kDa that was somewhat larger than the molecular weight of 24,555 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 26 kDa from which the secretory signal is considered to have been cleaved. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glutamine at position 20.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the mouse FGF binding protein (GenBank Accession No. U49641). Table 17 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the mouse FGF binding protein (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 21.2% in the entire region other than the N-terminal region. In particular, all the eight cysteine residues contained in the both proteins were conserved.

Table 17

```
HP                                MKFVPCLLLVTLSCLGTLGQAPRQKQGST
                                              ..**.  . .* . ...
MM MRLHSLILLSFLLLATQAFSEKVRKRAKNAPHSTAEEGVEGSAPSLGKAQNKQRSRTSKS
HP GEEFHFQTGGRDSCTMRPSSLGQGAGEVWLRVDCRNTDQTYWCEYRGQPSMCQAFAADPK
   .. .* * ....*  . ...... .. *.*.* ..**.. * . *.*. *   . * .
MM LTHGKFVTKDQATC---RWAVTEEEQGISLKVQCTQADQEFSCVFAGDPTDCLKHDKD-Q
HP SYWNQALQELRRLHHACQGA-PVLRPSVCREAGPQAHMQQVTSSLKGSPEPNQQPEAGTP
   **.*. ..**. .. *..* .**...***.  *..... *.....*...*... .. ..
MM IYWKQVARTLRKQKNICRDAKSVLKTRVCRKRFPESNLKLVNPNARGNTKPRKEKAEVSA
HP SLRPKATVKLTEATQLGKDSMEELGKAKPTTRPTAKPTQPGPRPGGNEEAKKKAWEHCWK
   . . *.   ......  *... .*. * . *. * . ..    *.  .. .*.* * * .
MM REHNKVQEAVSTEPNRIKEDI-TLNPAATQTM-TIRDPECLEDPDVLNQ-RKTALEFCGE
HP PFQALCAFLISFFRG
   .. ..*.*.......
MM SWSSICTFFLNMLQATSC
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA317400) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP02631> (SEQ ID Nos. 65, 75, and 85)

Determination of the whole base sequence of the cDNA insert of clone HP02631 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 42-bp 5'-untranslated region, a 147-bp ORF,

and a 1191-bp 3'-untranslated region. The ORF codes for a protein consisting of 48 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 25 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 10 kDa or less.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA156969) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP02632> (SEQ ID Nos. 66, 76, and 86)

Determination of the whole base sequence of the cDNA insert of clone HP02632 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 50-bp 5'-untranslated region, a 1116-bp ORF, and a 337-bp 3'-untranslated region. The ORF codes for a protein consisting of 371 amino acid residues and there existed eight putative transmembrane domains. Figure 26 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Caenorhabditis elegans hypothetical protein CELC2H12 (GenBank Accession No. U23169). Table 18 shows the comparison between amino acid sequences

of the human protein of the present invention (HP) and the C. elegans hypothetical protein CELC2H12 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 51.4% in the entire region.

Table 18

```
HP MAWTKYQLFLAGLMLVTGSINTLSAKWADNFMAEGCGGSKEHSFQHPFLQAVGMFLGEFS
         ...... .*.****.**..*****...*.      . .*.******. **.***
CE   MVAFAVIISVMMVVTGSLNTICAKWADSIKAD------GVPFNHPFLQATCMFFGEFL
HP CLAAFYL---------LRCRAAGQSDS-------SVDPQQPFNPLLFLPPALCDMTGTSL
   **..*.*         * ...*.*.*       .  . .****.**.******. ***.
CE CLVVFFLIFGYKRYVWNRANVQGESGSVTEITSEEKPTLPPFNPFLFFPPALCDILGTSI
HP MYVALNMTSASSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWLGILATIAGLVVVGLADLL
   **..**.*.*****************.**..*. ..   .*.*.* .. ***.**..*.
CE MYIGLNLTTASSFQMLRGAVIIFTGLLSVGMLNAQIKPFKWFGMLFVMLGLVIVGVTDIY
HP SKHDSQHKLSEVITGDLLIIMAQIIVAIQMVLEEKFVYKHNVHPLRAVGTEGLFGFVILS
    ..*. .. ...***.***.*********** *.*.. *..*..* *** *****.*.**
CE YDDDPLDDKNAIITGNLLIVMAQIIVAIQMVYEQKYLTKYDVPALFAVGLEGLFGMVTLS
HP LLLVPMYYIPAG-SFSGNPRGTLEDALDAFCQVGQQPLIAVALLGNISSIAFFNFAGISV
   .*..*.***..  .**.** * ***.. *. .....* **.** *.. ********.**
CE ILMIPFYYIHVPRTFSTNPEGRLEDVFYAWKEITEEPTIALALSGTVVSIAFFNFAGVSV
HP TKELSATTRMVLDSLRTVVIWALSLALGWEAFHALQILGFLILLIGTALYNGLHRPLLGR
   **************.**.***..*..*  * * *.*. ** .*..** .**..
CE TKELSATTRMVLDSVRTLVIWVVSIPLFHEKFIAIQLSGFAMLILGTLIYNDILIGPWFR
HP LSRGRPLAEESEQERLLGGTRTPINDAS

CE RNILPNLSSHANCARCWLCICGGDSELIEYEQEDQEHLMEA
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. N50907) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10488> (SEQ ID Nos. 67, 77, and 87)

Determination of the whole base sequence of the cDNA insert of clone HP10488 obtained from cDNA library of human liver revealed the structure consisting of a 39-bp 5'-untranslated region, a 273-bp ORF, and a 421-bp 3'-untranslated region. The ORF codes for a protein consisting of 90 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 27 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 10 kDa that was almost identical with the molecular weight of 10,151 predicted from the ORF. When expressed in COS7 cells, an expression product of about 6 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H73534) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10538> (SEQ ID Nos. 68, 78, and 88)

Determination of the whole base sequence of the cDNA insert of clone HP10538 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 357-bp 5'-untranslated region, a 1500-bp ORF, and a 1911-bp 3'-untranslated region. The ORF codes for a protein consisting of 499 amino acid residues and there existed at least four putative transmembrane domains. Figure 28 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the mouse pore-forming K^+ channel subunit (GenBank Accession No. AF056492). Table 19 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the mouse pore-forming K^+ channel subunit (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 32.4% in the N-terminal region of 241 amino acid residues.

Table 19

```
HP    MVDRGPLLTSAIIFYLAIGAAIFEVLEEPHWKEAKKNYYTQKLHLLKEFPCLGQEGLDK
           * . ...**. ** .*..**.** ..*.*.    . ..*.. **..*..*..
MM   MRSTTLLALLALVLLYLVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLED
HP   ILEVVSDAAGQG-----VAITGNQTFNNWNWPNAMIFAATVITTIGYGNVAPKTPAGRLF
     ..... .* * *      .....  ..**  .*..*..*.********.. .* *****
MM   FIKLLVEALGGGANPETSWTNSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGRLF
HP   CVFYGLFGVPLCLTWISALGKFFGGRAKR----LGQFLTKRGVSLRKAQITCTVIFIVWG
     *.**.* *.**    ....*. .*.. .*    ..... *. *.   ..  ..*.*.. *
MM   CIFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIG
HP   VLVHLVIPPFVFMVTEGWNYIEGLYYSFITISTIGFGDFVAGVNPSANYHALYRYFVELW
      *. ...*.***   *.*. .*..*. ..*..*.****.*.* . ...  . *. .* .*
MM   CLLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVPG-DGTGQNSPAYQPLVWFW
HP   IYLGLAWLSLFVNWKVSMFVEVHKAIKKRRRRRKESFESSPHSRKALQVKGSTASKDVNI
     * .***...
MM   ILFGLAYFASVLTTIGNWLRAVSRRTRAEMGGLTAQAASWTGTVTARVTQRTGPSAPPPE
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R25184) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10542> (SEQ ID Nos. 69, 79, and 89)

Determination of the whole base sequence of the cDNA insert of clone HP10542 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 23-bp 5'-untranslated region, a 321-bp ORF, and a 426-bp 3'-

untranslated region. The ORF codes for a protein consisting of 106 amino acid residues and there existed one putative transmembrane domain. Figure 29 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 12 kDa that was almost identical with the molecular weight of 11,724 predicted from the ORF. When expressed in COS7 cells, an expression product of about 13 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA029683) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10571> (SEQ ID Nos. 70, 80, and 90)

Determination of the whole base sequence of the cDNA insert of clone HP10571 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 95-bp 5'-untranslated region, a 459-bp ORF, and a 675-bp 3'-untranslated region. The ORF codes for a protein consisting of 152 amino acid residues and there existed one putative transmembrane domain. Figure 30 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 20 kDa that was larger than the molecular weight of 17,062 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 23 kDa

which is considered to have a sugar chain being attached after secretion. In addition, there exists in the amino acid sequence of this protein one site at which N-glycosylation may occur (Asn-Ile-Thr at position 10).

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA105822) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP01470> (SEQ ID Nos. 91, 101, and 111)

Determination of the whole base sequence of the cDNA insert of clone HP01470 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 157-bp 5'-untranslated region, a 1077-bp ORF, and a 385-bp 3'-untranslated region. The ORF codes for a protein consisting of 358 amino acid residues and there existed one putative transmembrane domain. Figure 31 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 43 kDa that was somewhat larger than the molecular weight of 40,489 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 40 kDa from which the secretory signal is considered to have been cleaved and a product of 43.5 kDa which is considered to have been subjected to some modification. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glycine at position 23. When

expressed in COS7 cells, an expression product of about 44 kDa was observed in the supernatant fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Caenorhabditis elegans hypothetical protein 39.9 kDa (SWISS-PROT Accession No. Q10005). Table 20 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the C. elegans hypothetical protein 39.9 kDa (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 58.9% in the entire region.

Table 20

```
HP MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIKKAYRKLALQLHPDRNPDD
                         *.. *  **********...*. ..********* .******.**
CE  MRILNVSLLVLASSLVAFVECGRDFYKILGVAKNANANQIKKAYRKLAKELHPDRNQDD
HP PQAQEKFQDLGAAYEVLSDSEKRKQYDTYGEEGL--KDGHQSSHGDIFSHFFGDFGFMFG
    *.******..*******.***  ** .****.  ..*  ..  * ** ***** *  *
CE EMANEKFQDLSSAYEVLSDKEKRAMYDRHGEEGVAKMGGGGGGHDPFSSFFGDF-FG-G
HP GTPRQQDRNIPRGSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTT
   *. .  . ..*.*.*...** *******.*.***. *.*.* .*..*.*.****.****.
CE GGGHGGEEGTPKGADVTIDLFVTLEEVYNGHFVEIKRKKAVYKQTSGTRQCNCRHEMRTE
HP QLGPGRFQMTQEVVCDECPNVKLVNEERTLEVEIEPGVRDGMEYPFIGEGEPHVDGEPGD
   *.*.***** *  ***********.*...****.* *. .* .  * ******..*.***
CE QMGQGRFQMFQVKVCDECPNVKLVQENKVLEVEVEVGADNGHQQIFHGEGEPHIEGDPGD
HP LRFRIKVVKHPIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVHISRDKITRPGAK
   *.*.*.. *** ***.************ ..* ****.* ***** *.. ***.*.***.
CE LKFKIRIQKHPRFERKGDDLYTNVTISLQDALNGFEMEIQHLDGHIVKVQRDKVTWPGAR
HP LWKKGEGLPNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQ-KVYNGLQG
   *.**.**.*....** ** *..****.***..*..*... * ..*.*..*. *.****
CE LRKKDEGMPSLEDNNKKGMLVVTFDVEFPKTELSDEQKAQIIEILQQNTVKPKAYNGL
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA282838) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP02419> (SEQ ID Nos. 92, 102, and 112)

Determination of the whole base sequence of the cDNA insert of clone HP02419 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 253-bp 5'-untranslated region, a 681-bp ORF, and a 1120-bp 3'-untranslated region. The ORF codes for a protein consisting of 226 amino acid residues and there existed four putative transmembrane domains. Figure 32 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human hypothetical protein KIAA0108 (SWISS-PROT Accession No. Q15012). Table 21 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human hypothetical protein KIAA0108 (KI). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 43.9% in the entire region.

Table 21

```
HP     MKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVVLLILLSALADPD---QY
                 ****..** *********.**.**...* .. ..*  ....*.   .
KI MVSMSFKRNRSDRFYSTRCCGCCHVRTGTIILGTWYMVVNLLMAILLTVEVTHPNSMPAV
HP NFSSSELGGDFEF-MDDANMCIAIAISLLMILICAMATYGAYKQRAAWIIPFFCYQIFDF
   *.  . .*. ..  . ..* *. .*.*.**..*..* .*** . ...*.******..***
KI NIQYEVIGNYYSSERMADNACVLFAVSVLMFIISSMLVYGAISYQVGWLIPFFCYRLFDF
HP ALNMLVAITVLIYPNSIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGYL
   .*. ****. *.*  .*.**. ** *.***.**.......**..*.*.*......**.**
KI VLSCLVAISSLTYLPRIKEYLDQL-PDFPYKDDLLALDSSCLLFIVLVFFALFIIFKAYL
HP ISCVWNCYRYINGRNSSDVLVYVT-SNDTTVLLPPYDDATVNGAAKEPPPPYVSA
   *.******.***.** ... ** . .. .  .**.* . .*. ..*******..*
KI INCVWNCYKYINNRNVPEIAVYPAFEAPPQYVLPTY-EMAVKMPEKEPPPPYLPA
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA173214) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP02631> (SEQ ID Nos. 93, 103, and 113)

Determination of the whole base sequence of the cDNA insert of clone HP02631 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 42-bp 5'-untranslated region, a 588-bp ORF, and a 750-bp 3'-untranslated region. Although the 49th amino acid residue is encoded by a stop codon, it is likely that this codon encodes selenocysteine from the molecular weight

of the translation product and the sequence comparison data with the Caenorhabditis elegans homologue. The ORF codes for a protein consisting of 195 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the intermediate region. Figure 33 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 58 kDa. In this case, the addition of a microsome led to the formation of a product of 56 kDa from which the secretory signal is considered to have been cleaved. Since both of these products are larger than the molecular weight of 22 kDa predicted from the ORF, it is likely that the protein interacts with another protein.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Caenorhabditis elegans hypothetical protein C35C5.3 (EMBL Accession No. Z78417). Table 22 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the C. elegans hypothetical protein C35C5.3 (CE). U at position 49 in the amino acid sequence of the protein of the present invention represents selenocysteine. Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 37.9% in the entire region other than the N-terminal region. Cystein was found in the sequence of the C. elegans protein at the posistion corresponding to position 49 encoded by the stop codon (selenocysteine) of the protein of the present invention.

Table 22

```
HP                                                  MRLLLL

CE MRIHDELQKQDMSRFGVFIIGVLFFMSVCDVLRTEEHSHDENHVHEKDDFEAEFGDETDS
HP LLVAASAMVRSEASANLGGVPSKRLKMQYATGPLLKFQICVSUGYRRVFEEYMRVISQRY
                                     * *..  *** **...*...    ...*

CE QSFSQGTEEDHIEVREQSSFVKPTAVHHAKDLPTLRIFYCVSCGYKQAFDQFTTFAKEKY
HP PDIRIEGENYLPQPIYRHIASFLSVFKLVLIGLIIVGKDPFAFFGMQAPSIWQWGQENKV
   *...***.*. *      ..*  **  *.... *.. * .**. **.  * * * ...**.

CE PNMPIEGANFAPVLWKAYVAQALSFVKMAVLVLVLGGINPFERFGLGYPQILQHAHGNKM
HP YACMMVFFLSNMIENQCMSTGAFEITLNDVPVWSKLESGHLPSMQQLVQILDNEMKLNVH
    .**.**.*.*..*.  ;******. *.. ..***.***..** *...*..*... .

CE SSCMLVFMLGNLVEQSLISTGAFEVYLGNEQIWSKIESGRVPSPQEFMQLIDAQLAVLGK
HP MDSIPHHRS

CE APVNTESFGEFQQTV
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA156969) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP02695> (SEQ ID Nos. 94, 104, and 114)

Determination of the whole base sequence of the cDNA insert of clone HP02695 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 112-bp 5′-untranslated region, a 1020-bp ORF, and a 160-bp 3′-untranslated region. The ORF codes for a protein consisting of 339 amino acid residues and there existed three putative transmembrane domains. Figure 34 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 38 kDa that was almost identical with the molecular weight of 38,274 kDa predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the rat hypertension-induced protein S-2 fragment (PIR Accession No. 539959). Table 23 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the rat hypertension-induced protein S-2 fragment (RN). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 74.3% in the entire region.

Table 23

```
HP MNWELLLWLLVLCALLLLLVQLLRFLRADGDLTLLWAEWQGRRPEWELTDMVVWVTGASS

HP GIGEELAYQLSKLGVSLVLSARRVHELERVKRRCLENGNLKEKDILVLPLDLTDTGSHEA
                                ****.*****************.**.**.
RN                              VKRRSLENGNLKEKDILVLPLDLADTSSHDI
HP ATKAVLQEFGRIDILVNNGGMSQRSLCMDTSLDVYRKLIELNYLGTVSLTKCVLPHMIER
   ***.****************... **  .*..*... ***.*********** ****.**
RN ATKTVLQEFGRIDILVNNGGVAHASLVENTNMDIFKVLIEVNYLGTVSLTKCFLPHMMER
HP KQGKIVTVNSILGIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIVSNICPGPVQSN
   .*****...*
RN NQGKIVVMKS
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T84331) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10031> (SEQ ID Nos. 95, 105, and 115)

Determination of the whole base sequence of the cDNA insert of clone HP10031 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 55-bp 5'-untranslated region, a 1464-bp ORF, and a 649-bp 3'-untranslated region. The ORF codes for a protein consisting of 487 amino acid residues and there existed eleven putative transmembrane domains. Figure 35 depicts the hydrophobicity/hydrophilicity profile, obtained

by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight. When expressed in COS7 cells, an expression product of about 55 kDa was observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Caenorhabditis elegans hypothetical protein CELK07H8 (GenBank Accession No. AF047659). Table 24 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the C. elegans hypothetical protein CELK07H8 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 44.2% in the entire region.

Table 24

```
HP                               MDGTETRQRRLDSCGKPGELGLPHPLSTGGLPVAS

CE MKGGGGIGDGKKDYQSAVHEGLTTFDQLGIALEDVGKSMDAETATPGGSLFSRVIFRFRN
HP EDGALRAPESQSVTPKPLETEPSRETAWSIGLQVTVPFMFAGLGLSWAGMLLDYFQHWPV
   *...*.... .  .     .  . *... . .** **  ****. .**..*.     **.
CE ENSSLKSRTYDHSNDLVNMSVIPAESSYVLFFQVLFPFAVAGLGMVFAGLVLSIVVTWPL
HP FVEVKDLLTLVPPLVGLKGNLEMTLASRLSTAANTGQIDDPQEQHRVISSNLALIQVQAT
   * *.  ..*.***.*.**************** ** *..*...... *. .****.*****
CE FEEIPEILILVPALLGLKGNLEMTLASRLSTLANLGHMDSSKQRKDVVIANLALVQVQAT
HP VVGLLAAVAALLLGVVSREEVDVAKVELLCASSVLTAFLAAFALGVLMVCIVIGARKLGV
   **..**.. *  *. ..... * *. .*.****. **  *...*..*** .....** ..
CE VVAFLASAFAAALAFIPSGDFDWAHGALMCASSLATACSASLVLSLLMVVVIVTSRKYNI
HP NPDNIATPIAASLGDLITLSILALVSSFFYR-HKDSRYLTPLVCLSFAALTPVWVLIAKQ
   ****.***********.**..**. .* * . *.....*. .* . *  * * *. **..
CE NPDNVATPIAASLGDLTTLTVLAFFGSVFLKAHNTESWLNVIVIVLFLLLLPFWIKIANE
HP SPPIVKILKFGWFPIILAMVISSFGGLILSKTVSKQQYKGMAIFTPVICGVGGNLVAIQT
   .  . ..*  ** *.*..*.*** **.**...*  ..*.......**. ******.*.*.
CE NEGTQETLYNGWTPVIMSMLISSAGGFILETAV--RRYHSLSTYGPVLNGVGGNLAAVQA
HP SRISTYLHMWSAPGVLPLQ--MKKFWPNPCSTFCTSEINSMSARVLLLLVVPGHLIF-FY
   **.***.*. .. ****  .   ...* ..  ..* ..* .*.*************. * *
CE SRLSTYFHKAGTVGVLPNEWTVSRF-TSVQRAFFSKEWDSRSARVLLLLVVPGHICFNFL
HP I-IYLVEGQSVINSQ--TFVVLYLLAGLIQVTILLYLAEVMVRLTWHQALDPDNHCIPYL
   * .. ..... ....    *. **..*..***.***.. ...* * *.  .****  ****
CE IQLFTLTSKNNVTPHGPLFTSLYMIAAIIQVVILLFVCQLLVALLWKWKIDPDNSVIPYL
HP TGLGDLLGTGLLALCFFTDWLLKSKAELGGISELASGPP
   *.**********  . *.*
CE TALGDLLGTGLLFIVFLTTDHFDPKELTSS
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for

example, Accession No. AA334000) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10530> (SEQ ID Nos. 96, 106, and 116)

Determination of the whole base sequence of the cDNA insert of clone HP10530 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 80-bp 5'-untranslated region, a 1182-bp ORF, and a 95-bp 3'-untranslated region. The ORF codes for a protein consisting of 393 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 36 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 46 kDa that was somewhat larger than the molecular weight of 44,912 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 45.5 kDa from which the secretory signal is considered to have been cleaved. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from lysine at position 23. When expressed in COS7 cells, an expression product of about 43 kDa was observed in the supernatant fraction and the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Arabidopsis thaliana hypothetical protein IG002N01 (GenBank Accession No. AF007269). Table 25 shows the comparison between amino acid sequences of the

human protein of the present invention (HP) and the A. thaliana hypothetical protein IG002N01 (AT). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 27.0% in the N-terminal region of 355 amino acid residues.

Table 25

```
HP                                                    MRTLFNLLWL

AT MELTSPQKSPSSNDVVSFSVSLVRNSMARRRRSSAAESLKRRNDGYESLCQVVQQDSDRR
HP ALACSPVHTTLSKSDAKKAASKTLLEKSQFSDKPVQDRGLVVTDLKAESVVLEHRSYCSA
                                 ........*.* **.. .... **..  ..
AT LITIFVIFFIVIPAVSIAVYKVKFADRVIQTESSIRQKGIVKTDINFQEILTEHSK--AS
HP KARDRHFAGDVLGYVTPWNSHGYDVTKVFGSKFTQISPVWLQ-LKRRGREMFEVTGLHDV
   ....**..  **.*.**  ..* ..  *....  . .  *.* *..**... . .**...
AT ENSTRHYDYPVLAYITP--CQGSGL--VLEGR-HNADKGWIQELRSRGNALSASKGLPKL
HP DQGWMRAVRKHAKGLHIVPRLLFEDWTYDDFRNVLDSEDEIEELSKTVVQVAKNQHFDGF
       . . . . * ... .  * .  **  .. .*.*  *.*  . ..  .. . ... .
AT ---YNSCIFHALKRMNFFTLELVNFNTYLVIMFALNS-REMEYNGIVLESWSRWAAYGVL
HP VVEVWNQLLSQKRVGLIHMLTHLAEALHQARLLALLVIPPAITPGTDQLGMFTHKEFEQL
        ...  .    * . *   ... .... .... .  .  ... *.  *...... *
AT HDPDLRKMALKFVKQLGDALHSTSSPRNNQQHMQFMYVVGPPRSEKLQMYDFGPEDLQFL
HP APVLDGFSLMTYDYSTAHQPGPNAPLSWVRACVQ-VLDPKSK----WRSKILLGLNFYGM
      .*********.*....******..*.   .. .*.....      .*.***.****
AT KDSVDGFSLMTYDFSNPQNPGPNAPVKWIDLTLKLLLGSSNNIDSNIARKVLLGINFYGN
HP DYATSKDAREPVVGARYIQTLKDHRPRMVWDSQASEHFFEYKKSRSGRHVVFYPTLKSLQ
   *...* .. ....*  *.. *..*.* . **....**.* *..... .*.******.*.
AT DFVISGGGGGAITGRDYLALLQKHKPTFRWDKESGEHLFMYRDDKNIKHAVFYPTLMSIL
HP VRLELARELGVGVSIWELGQGLDYFYDLL
   .*** **  *.*.****.**. ..*
AT LRLENARLWGIGISIWEIGQDKGHFGKYAEASLEASSIFSGHTFDMQFRTNPRQLSRNGS
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA302913) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the

THI[illegible] (USPTO)

THIS PA[illegible] (USPTO)

protein of the present invention.

<HP10541> (SEQ ID Nos. 97, 107, and 117)

Determination of the whole base sequence of the cDNA insert of clone HP10541 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 7-bp 5'-untranslated region, a 591-bp ORF, and a 113-bp 3'-untranslated region. The ORF codes for a protein consisting of 196 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 37 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 23 kDa that was somewhat larger than the molecular weight of 21,553 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 20 kDa from which the secretory signal is considered to have been cleaved and a product of 23 kDa which is considered to have a sugar chain being attached. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glycine at position 41. In addition, there exists in the amino acid sequence of this protein one site at which N-glycosylation may occur (Asn-Leu-Thr at position 185).

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human zymogen membrane protein (GenBank Accession No. AF056492). Table 26 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human zymogen membrane protein (ZM). Therein, the marks of -, *, and . represent a

gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 37.6% in the C-terminal region of 133 amino acid residues.

Table 26

```
HP MWRVPGTTRRPVTGESPGMHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFS-TTEDYD
                                              **.**** ** .... *
ZM               MLTVALLALLCASASGNAIQARSSSYSGEYGSGGGKRFSHSGNQLD
HP HEITGLRVSVGLLLVKSVQVKLGDSWDVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLR
     **.***.*.   . ..**. *. *.  .*. .*. .*. *.*** ...*   .. .*.
ZM GPITALRVRVNTYYIVGLQVRYGKVWSDYVGGRNGDLEEIFLHPGESVIQVSGKYKWYLK
HP GMVMYTSKDRYFYFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIKSIGFEWN-YPLEEP
    .*. *.*.**. *** .*   .* * . . **  * *.   * *..**..*. **
ZM KLVFVTDKGRYLSFGKDSGTSFNAVPLHPNTVLRFISGRSGSL-IDAIGLHWDVYPTSCS
HP TTEPPVNLTYSANSPVGR

ZM RC
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA340605) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10550> (SEQ ID Nos. 98, 108, and 118)

Determination of the whole base sequence of the cDNA

insert of clone HP10550 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 241-bp 5'-untranslated region, a 324-bp ORF, and a 86-bp 3'-untranslated region. The ORF codes for a protein consisting of 107 amino acid residues and there existed one putative transmembrane domain. Figure 38 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA348310) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10590> (SEQ ID Nos. 99, 109, and 119)

Determination of the whole base sequence of the cDNA insert of clone HP10590 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 77-bp 5'-untranslated region, a 1053-bp ORF, and a 180-bp 3'-untranslated region. The ORF codes for a protein consisting of 350 amino acid residues and there existed one putative transmembrane domain. Figure 39 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 40 kDa that was almost identical with the molecular weight of 39,285 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of

43 kDa which is considered to have a sugar chain being attached. In addition, there exist in the amino acid sequence of this protein two sites at which N-glycosylation may occur (Asn-Asn-Ser at position 144 and Asn-Leu-Thr at position 328).

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA461346) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10591> (SEQ ID Nos. 100, 110, and 120)

Determination of the whole base sequence of the cDNA insert of clone HP10591 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 232-bp 5'-untranslated region, a 324-bp ORF, and a 844-bp 3'-untranslated region. The ORF codes for a protein consisting of 107 amino acid residues and there existed one putative transmembrane domain. Figure 40 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 12 kDa that was almost identical with the molecular weight of 11,328 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H09424) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein

of the present invention.

<HP01462> (SEQ ID Nos. 121, 131, and 141)

Determination of the whole base sequence of the cDNA insert of clone HP01462 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 121-bp 5'-untranslated region, a 1452-bp ORF, and a 477-bp 3'-untranslated region. The ORF codes for a protein consisting of 483 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 41 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 72 kDa that was larger than the molecular weight of 55,838 predicted from the ORF. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from lysine at position 21.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Caenorhabditis elegans hypothetical protein ZK1058.4 (EMBL Accession No. Z35604). Table 27 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the C. elegans hypothetical protein ZK1058.4 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 35.6% in the entire region.

Table 27

```
HP MKAFHTFCVVLLVFGSVSEAKFDDFEDEEDIVEYDDNDFAEFEDVMEDSVTESPQRVIIT
                                                          * *
CE                                          MKIVWIFLIFFIGFAIST
HP EDDE-DETTVELEGQDENQEGDFEDADTQEGDTESEPYDDEEFEGYEDKP---------D
   .*.* .* . *. * ...*. ... ....   .... ...*.*.  *..*         *
CE DDNEFAEFEDEFVGSSATQAPEIQREGEPPVLKQKDDFEEEDFGVVEEEPEEAEKVREAD
HP TSSSKNKDPITIVDVPAHLQNSWESYYLEILMVTGLLAYIMNYIIGKNKNSRLAQAWFNT
   ....   .*....*****....*.** .* ..*  .* *. **.***..*...**. *.
CE SDDAAPAQPLKFADVPAHFRSNWASYQVEGIVVLIILIYMTNYLIGKTTNASIAQTIFDM
HP HRELLESNFTLVGDDGTNKEATSTGKLNQENEHIYNLWCSGRVCCEGMLIQLRFLKRQDL
    *  **..*..******.. .. . .*..... ... **.***  .....*....****.
CE CRPTLEEQFAVVGDDGTTDLDKMIPSLKHDTDSTFSAWCTGRVNVNSLFLQMKMVKRQDV
HP LNVLARMMRPVSDQVQIKVTMN-DEDMDTYVFAVGTRKALVRLQKEMQDLSEFCSDKPKS
   .. .  *. * .*.. **.... ..* *. .****..*   .  *** **..* *.. ..
CE VSRIMEMFTPSGDKMTIKASLETTNDTDPLIFAVGEKKIASKYFKEMLDLNSFASERKQA
HP GAKYGLPDSLAILSEMGEVTDGMMDTKMVHFLTHYADKIESVHFSDQFSGPKIMQEEGQP
   .....**.* .. .. .**. ...*. .* .*....* ** .*.****.***  ..*. .
CE AQQFNLPASWQVYADQNEVVFSILDPGVVSLLKKHEDAIEFIHISDQFTGPKPAEGESYT
HP LKLPDTKRTLLFTFNVPGSGNTYPKDMEALLPLMNMVIYSIDKAKKFRLNREGKQKADKN
    .**...* .. ..*..  *    .* *... ..*.*.* ****.*..*....* **...
CE -RLPEAQRYMFVSLNLQYLG----QDEESVMEILNLVFYLIDKARKMKLSKDAKVKAERR
HP RARVEENFLKLTHVQRQEAAQSRREEKKRAEKERIMNEEDPEKQRRLEEAALRREQKKLE
   *   *..*** **  ******.*****.*.  *...*.*.***.*.***. .*.**.*
CE RKEFEDAFLKQTHQFRQEAAQARREEKTRERKQKLMDESDPERQKRLEAKELKREAKA--
HP KKQMKMKQIKVKAM
    *  ****.***
CE -KSPKMKQLKVK
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for

example, Accession No. AA307793) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP02485> (SEQ ID Nos. 122, 132, and 142)

Determination of the whole base sequence of the cDNA insert of clone HP02485 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 69-bp 5'-untranslated region, a 1005-bp ORF, and a 1672-bp 3'-untranslated region. The ORF codes for a protein consisting of 334 amino acid residues and there existed one putative transmembrane domain. Figure 42 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 36 kDa that was almost identical with the molecular weight of 38,171 predicted from the ORF. When expressed in COS7 cells, an expression product of about 23 kDa was observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Caenorhabditis elegans hypothetical protein W01A11.2 (GenBank Accession No. U64852). Table 28 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the C. elegans hypothetical protein W01A11.2 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 45.5% in the entire region.

Table 28

```
HP                          MVEFAPLFMPWERRLQTLAVLQFVFSFLALAEICT-V
                             .***..**.***.****. *.* .. *. .    *
CE MRLRLSSISGKAKLPDKEICSSVSRILAPLLVPWKRRLETLAVMGFIFMWVILPIMDLWV
HP GFIALLFTRFWLLTVLYAAWWYLDRDKPRQGGRHIQAIRCWTIWKYMKDYFPISLVKTAE
    * .*. **.*.*. ***.*.* * *.*....*. .   *  . ***. .***..*.***.
CE PFHVLFNTRWWFLVPLYAVWFYYDFDTPKKASRRWNWARRHVAWKYFASYFPLRLIKTAD
HP LDPSRNYIAGFHPHGVLAVGAFANLCTESTGFSSIFPGIRPHLMMLTLWFRAPFFRDYIM
    * ..**** * ****...**.*....*..***.. ****..*.* *.   *  ** *.. .
CE LPADRNYIIGSHPHGMFSVGGFTAMSTNATGFEDKFPGIKSHIMTLNGQFYFPFRREFGI
HP SAGLVTSEKESAAHILNRKGGGNLLGIIVGGAQEALDARPGSFTLLLRNRKGFVRLALTH
     * .. .*** ...*.. * *.  .*..*** ***.*.*.. ** * **.** . **.
CE MLGGIEVSKESLEYTLTKCGKGRACAIVIGGASEALEAHPNKNTLTLINRRGFCKYALKF
HP GAPLVPIPSFGENDLFDQIPNSSGSWLRYIQNRLQKIMGISLPLFHGRGVF-QYSFGLIP
   ** ***...******..*  *..**.** .*.......*.. **..**..* ** .**.*
CE GADLVPMYNFGENDLYEQYENPKGSRLREVQEKIKDMFGLCPPLLRGRSLFNQYLIGLLP
HP YRRPITTVVGKPIEVQKTLHPSEEEVNQLHQRYIKELCNLFEAHKLKFNIPADQHLEFC
   .*.*.***.*.** * .* .*. *....**..* ..*.****..*   .**.* ** *
CE FRKPVTTVMGRPIRVTQTDEPTVEQIDELHAKYCDALYNLFEEYKHLHSIPPDTHLIFQ
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. D25664) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP02798> (SEQ ID Nos. 123, 133, and 143)

Determination of the whole base sequence of the cDNA

insert of clone HP02798 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 31-bp 5'-untranslated region, a 804-bp ORF, and a 301-bp 3'-untranslated region. The ORF codes for a protein consisting of 267 amino acid residues and there existed four putative transmembrane domains. Figure 43 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 29 kDa that was almost identical with the molecular weight of 30,778 predicted from the ORF. When expressed in COS7 cells, an expression product of about 26 kDa was observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human DHHC-containing cysteine-rich protein (GenBank Accession No. U90653). Table 29 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human DHHC-containing cysteine-rich protein (DH). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 35.0% in the intermediate region of 100 amino acid residues. The positions of seven cysteines were conserved between the two proteins. The protein of the present invention also had the DHHC (Asp-His-His-Cys) sequence.

Table 29

```
HP                                           MAPWALLSPGVLVRTGHTVLTWGI

DH MYKMNICNKPSNKTAPEKSVWTAPAQPSGPSPELQGQRSRRNGWSWPPHPLQIVAWLLYL
HP TLVLFLHDTELRQWEEQGELLLPLTFLLLVLGSLLLYLAVSLMDPGYVNVQPQP-QEELK
                                           * *...*..  .**.  .**. .. .. *
DH FFAVIGFGILVPLLPHHWVPAGYACMGAIFAGHLVVHLTAVSIDPADDNVRDKSYAGPLP
HP EEQTAMVPPAIPLRRCRYCLVLQPLRARHCRECRRCVRRYDHHCPWMENCVGERNHPLFV
   . .  ...*   .*. * *  . *..**..*..**  .**** *..*******..**.
DH IFNRSQHAHVIEDLHCNLCNVDVSARSKHCSACNKCVCGFDHHCKWLNNCVGERNYRLFL
HP VYLALQLVVLLWGLYLAWSGLRFFQPWGLWLRSSGLLFATFLLLSLFSLVASLLLVSHLY
   .* .*. .*
DH HSVASALLGVLLLVLGGHICLRGVLCQPHASAHQPTL
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. D79050) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10041> (SEQ ID Nos. 124, 134, and 144)

Determination of the whole base sequence of the cDNA insert of clone HP10041 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 12-bp 5'-untranslated region, a 321-bp ORF, and a 286-bp 3'-untranslated region. The ORF codes for a protein consisting of 106 amino acid residues and there existed one putative transmembrane domain. Figure 44 depicts

the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 12 kDa that was almost identical with the molecular weight of 12,060 predicted from the ORF. When expressed in COS7 cells, an expression product of about 13 kDa was observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Caenorhabditis elegans hypothetical protein K10B2.4 (GenBank Accession No. U28730). Table 30 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the C. elegans hypothetical protein K10B2.4 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 62.1% in the entire region.

Table 30

```
HP MSTNNMSDPRRPNKVLRYKP---PPSECNPALDDPTPDYMNLLGMIFSMCGLMLKLKWCA
         .****.*...****    .... ..   .** *.***.***********...***.
CE   MQQNGDPRRTNRIVRYKPLDSTANQQQAISEDPLPEYMNVLGMIFSMCGLMIRMKWCS
HP WVAVYCSFISFANSRSSEDTKQMMSSFMLSISAVVMSYLQNPQPMTPPW
   *.*..** *****.*.*.*.**..******.*********** *..***
CE WLALVCSCISFANTRTSDDAKQIVSSFMLSVSAVVMSYLQNPSPIIPPWVTLLQS
```

Furthermore, the search of the GenBank using the base

sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H20098) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10246> (SEQ ID Nos. 125, 135, and 145)

Determination of the whole base sequence of the cDNA insert of clone HP10246 obtained from cDNA library of human epidermoid carcinoma cell line KB revealed the structure consisting of a 110-bp 5'-untranslated region, a 675-bp ORF, and a 79-bp 3'-untranslated region. The ORF codes for a protein consisting of 224 amino acid residues and there existed five putative transmembrane domains. Figure 45 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 23 kDa that was somewhat smaller than the molecular weight of 25,244 predicted from the ORF. When expressed in COS7 cells, an expression product of about 21 kDa was observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human putative seven transmembrane domain protein (GenBank Accession No. Y18007). Table 31 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human putative seven transmembrane domain protein (TM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that

of the protein of the present invention, respectively. The both proteins shared a homology of 93.3% in the entire region.

Table 31

```
HP MTLFHFGNCFALAYFPYFITYKCSGLSEYNAFWKCVQAGVTYLFVQLCKMLFLATFFPTW
   ***********************..***********************************
TM MTLFHFGNCFALAYFPYFITYKCTDLSEYNAFWKCVQAGVTYLFVQLCKMLFLATFFPTW
HP EGGIYDFIGEFMKASVDVADLIGLNLVMSRNAGKGEYKIMVAALGWATAELIMSRCIPLW
   ************************************************************
TM EGGIYDFIGEFMKASVDVADLIGLNLVMSRNAGKGEYKIMVAALGWATAELIMSRCIPLW
HP VGARGIEFDWKYIQMSIDSNISLVHYIVASAQVWMITRYDLYHTFRPAVLLLMFLSVYKA
   *********************** .******************************.****
TM VGARGIEFDWKYIQMSIDSNISLGPYIVASAQVWMITRYDLYHTFRPAVLLLMFLRVYKA
HP FVMETFVHLCSLGSWAALLARAVVTGLLALSTLALYVAVVNVHS
   ****************.*.* .**.***....**.*********
TM FVMETFVHLCSLGSWAVLMAGVVVKGLLVIRNLAMYVAVVNVHS
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA453931) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10392> (SEQ ID Nos. 126, 136, and 146)

Determination of the whole base sequence of the cDNA insert of clone HP10392 obtained from cDNA library of human osteosarcoma cell line U-2 OS revealed the structure

consisting of a 24-bp 5'-untranslated region, a 777-bp ORF, and a 726-bp 3'-untranslated region. The ORF codes for a protein consisting of 258 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 46 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 34 kDa that was somewhat larger than the molecular weight of 29,623 predicted from the ORF. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from leucine at position 49.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H15999) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention. In addition, partial identity with the hypothetical protein KIAA0384 (Accession No. AB002382) was observed, although the hypothetical protein had a different ORF.

<HP10489> (SEQ ID Nos. 127, 137, and 147)

Determination of the whole base sequence of the cDNA insert of clone HP10489 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 137-bp 5'-untranslated region, a 333-bp ORF, and a 189-bp 3'-untranslated region. The ORF codes for a protein consisting of 110 amino acid residues and there existed two putative transmembrane domains. Figure 47 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 19 kDa that was somewhat larger than the molecular weight of 12,010 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA262162) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10519> (SEQ ID Nos. 128, 138, and 148)

Determination of the whole base sequence of the cDNA insert of clone HP10519 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 67-bp 5'-untranslated region, a 276-bp ORF, and a 367-bp 3'-untranslated region. The ORF codes for a protein consisting of 91 amino acid residues and there existed one putative transmembrane domain. Figure 48 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 10 kDa that was almost identical with the molecular weight of 10,275 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. W16639) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein

of the present invention.

<HP10531> (SEQ ID Nos. 129, 139, and 149)

Determination of the whole base sequence of the cDNA insert of clone HP10531 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 55-bp 5'-untranslated region, a 1035-bp ORF, and a 1092-bp 3'-untranslated region. The ORF codes for a protein consisting of 344 amino acid residues and there existed five putative transmembrane domains. Figure 49 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R50695) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10574> (SEQ ID Nos. 130, 140, and 150)

Determination of the whole base sequence of the cDNA insert of clone HP10574 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 210-bp 5'-untranslated region, a 1287-bp ORF, and a 1276-bp 3'-untranslated region. The ORF codes for a protein consisting of 428 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the intermediate region. Figure 50 depicts the hydrophobicity/hydrophilicity profile, obtained

by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from serine at position 36.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Drosophila melanogaster GOLIATH protein (SWISS-PROT Accession No. Q06003). Table 32 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the D. melanogaster GOLIATH protein (DM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The intermediate region of 169 amino acids of the protein of the present invention shared a homology of 41.4% with the N-terminal region of the D. melanogaster GOLIATH protein.

Table 32

```
HP MGPPPGAGVSCRGGCGFSRLLAWCFLLALSPQAPGSRGAEAVWTAYLNVSWRVPHTGVNR
HP TVWELSEEGVYGQDSPLEPVAGVLVPPDGPGALNACNPHTNFTVPTVWGSTVQVSWLALI
HP QRGGGCTFADKIHLAYERGASGAVIFNFPGTRNEVIPMSHPGAVDIVAIMIGNLKGTKIL
                                                  .*.*... .  * ..
DM                                          MQLEKMQIKGKTRNIAAVITYQNIGQDLS
HP QSIQRGIQVTMVIEVGKK---HGPWVNHYSIFFVSVSFFIITAATVGYFIFYSARRLRNA
    ....* .**. *  *..     . .*. *..***.* **. .... ..***  .*.*
DM LTLDKGYNVTISIIEGRRGVRTISSLNRTSVLFVSIS-FIV-DDILCWLIFYYIQRFRYM
HP RAQSRKQRQLKADAKKAIGRLQLRTLKQGDKEIGPDGDSCAVCIELYKPNDLVRILTCNH
   .*.... *.* . .**** ... .* * .* * . *.*.**.*** ***.* .***.*.*
DM QAKDQQSRNLCSVTKKAIMKIPTKTGKFSD-EKDLDSDCCAICIEAYKPTDTIRILPCKH
HP IFHKTCVDPWLLEHRTCPMCKCDILKALGIEVDVEDGSVSLQVPVSNEISNSASSHEEDN
    ***.*.****.********* *.**  *  *.
DM EFHKNCIDPWLIEHRTCPMCKLDVLKFYGYVVGDQIYQTPSPQHTAPIASIEEVPVIVVA
HP RSETASSGYASVQGTDEPPLEEHVQSTNESLQLVNHEANSVAVDVIPHVDNPTFEEDETP

DM VPHGPQPLQPLQASNMSSFAPSHYFQSSRSPSSSVQQQLAPLTYQPHPQQAASERGRRNS
HP NQETAVREIKS

DM APATMPHAITASHQVTDV
```

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA155685) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

INDUSTRIAL APPLICABILITY

The present invention provides human proteins having hydrophobic domains, DNAs coding for these proteins, and expression vectors for these DNAs as well as eucaryotic cells expressing these DNAs. All of the proteins of the present invention are secreted or exist in the cell membrane, so that they are considered to be proteins controlling the proliferation and/or the differentiation of the cells. Accordingly, the proteins of the present invention can be employed as pharmaceuticals such as carcinostatic agents which act to control the proliferation and/or the differentiation of the cells, or as antigens for preparing antibodies against these proteins. The DNAs of the present invention can be utilized as probes for the genetic diagnosis and gene sources for the gene therapy. Furthermore, the DNAs can be utilized for large-scale expression of these proteins. Cells into which these genes are introduced to express these proteins, can be utilized for detection of the corresponding receptors and ligands, screening of novel low-molecular pharmaceuticals, and so on.

The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or

primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, Trends Pharmacol. Sci. 15(7): 250-254; Lavarosky et al., 1997, Biochem. Mol. Med. 62(1): 11-22; and Hampel, 1998, Prog. Nucleic Acid Res. Mol. Biol. 58: 1-39; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished

through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, Bioessays 14(9): 629-633; Zwaal et al., 1993, Proc. Natl. Acad. Sci. USA 90(16): 7431-7435; Clark et al., 1994, Proc. Natl. Acad. Sci. USA 91(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination, preferably detected by positive/negative genetic selection strategies (Mansour et al., 1988, Nature 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614, 396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s). Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25%(more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more

preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide, as determined by those of skill in the art. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous, or related to that encoded by the polynucleotides.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides

capable of hybridizing under reduced stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table 33 below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Table 33

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp)‡	Hybridization Temperature and Buffer†	Wash Temperature and Buffer†
A	DNA : DNA	≥50	65℃; 1×SSC -or- 42℃; 1×SSC,50% formamide	65℃; 0.3×SSC
B	DNA : DNA	<50	T_B*; 1×SSC	T_B*; 1×SSC
C	DNA : RNA	≥50	67℃; 1×SSC -or- 45℃; 1×SSC,50% formamide	67℃; 0.3×SSC
D	DNA : RNA	<50	T_D*; 1×SSC	T_D*; 1×SSC
E	RNA : RNA	≥50	70℃; 1×SSC -or- 50℃; 1×SSC,50% formamide	70℃; 0.3×SSC
F	RNA : RNA	<50	T_F*; 1×SSC	T_F*; 1×SSC
G	DNA : DNA	≥50	65℃; 4×SSC -or- 42℃; 4×SSC,50% formamide	65℃; 1×SSC
H	DNA : DNA	<50	T_H*; 4×SSC	T_H*; 4×SSC
I	DNA : RNA	≥50	67℃; 4×SSC -or- 45℃; 4×SSC,50% formamide	67℃; 1×SSC
J	DNA : RNA	<50	T_J*; 4×SSC	T_J*; 4×SSC
K	RNA : RNA	≥50	70℃; 4×SSC -or- 50℃; 4×SSC,50% formamide	67℃; 1×SSC
L	RNA : RNA	<50	T_L*; 2×SSC	T_L*; 2×SSC
M	DNA : DNA	≥50	50℃; 4×SSC -or- 40℃; 6×SSC,50% formamide	50℃; 2×SSC
N	DNA : DNA	<50	T_N*; 6×SSC	T_N*; 6×SSC
O	DNA : RNA	≥50	55℃; 4×SSC -or- 42℃; 6×SSC,50% formamide	55℃; 2×SSC
P	DNA : RNA	<50	T_P*; 6×SSC	T_P*; 6×SSC
Q	RNA : RNA	≥50	60℃; 4×SSC -or- 45℃; 6×SSC,50% formamide	60℃; 2×SSC
R	RNA : RNA	<50	T_R*; 4×SSC	T_R*; 4×SSC

‡: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

†: SSPE (1×SSPE is 0.15M NaCl, 10mM NaH_2PO_4, and 1.25mM EDTA, pH7.4) can be substituted for SSC (1×SSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_B - T_R: The hybridization temperature for hybrids anticipated to be less than

50 base pairs in length should be 5-10℃ less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(℃)=2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(℃)=81.5 + 16.6($\log_{10}$[Na^+]) + 0.41 (%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na^+] is the concentration of sodium ions in the hybridization buffer ([Na^+] for 1×SSC=0.165M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and Current Protocols in Molecular Biology, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25%(more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

CLAIMS

1. A protein comprising any one of an amino acid sequence selected from the group consisting of SEQ ID Nos. 1 to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130.

2. An isolated DNA coding for the protein according to Claim 1.

3. An isolated cDNA comprising any one of a base sequence selected from the group consisting of SEQ ID Nos. 11 to 20, 41 to 50, 71 to 80, 101 to 110, and 131 to 140.

4. The cDNA according to Claim 3 consisting of any one of a base sequence selected from the group consisting of SEQ ID Nos. 21 to 30, 51 to 60, 81 to 90, 111 to 120, and 141 to 150.

5. An expression vector that is capable of expressing the DNA according to any one of Claim 2 to Claim 4 by in vitro translation or in eucaryotic cells.

6. A transformed eucaryotic cell that is capable of expressing the DNA according to any one of Claim 2 to Claim 4 and of producing the protein according to Claim 1:

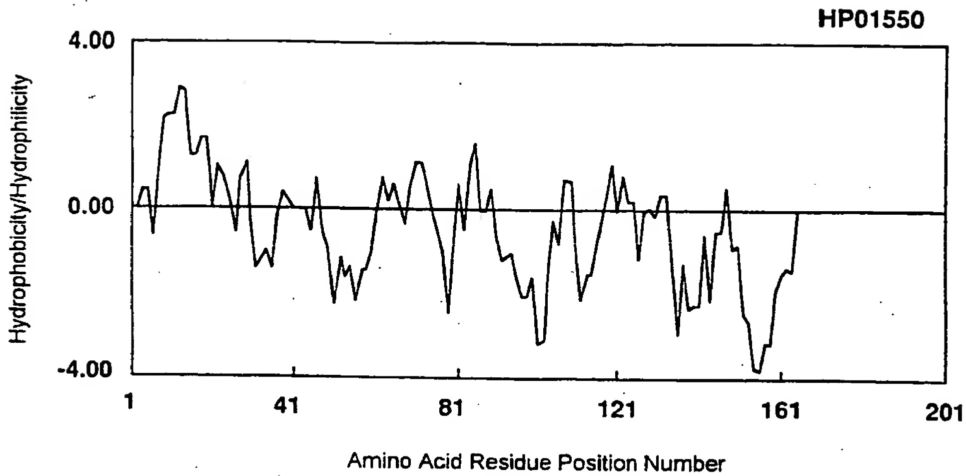

Fig. 1

WO 00/05367
2/50
PCT/JP99/03929

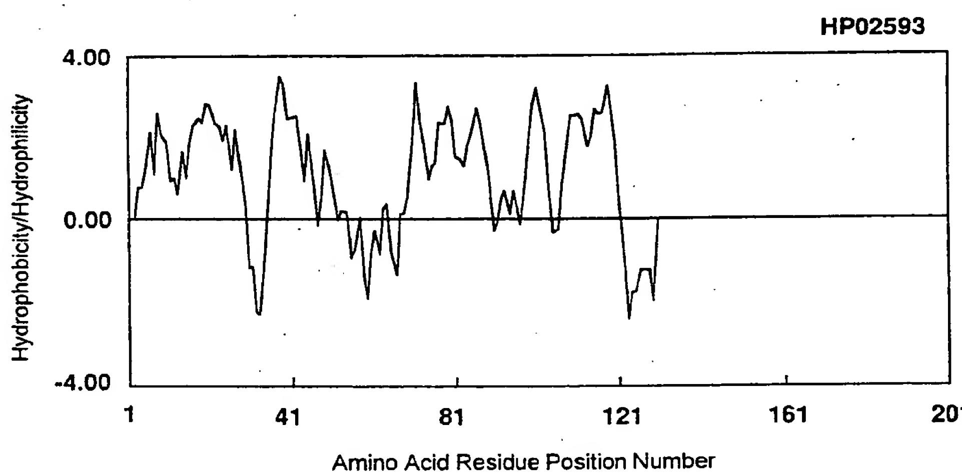

Fig. 2

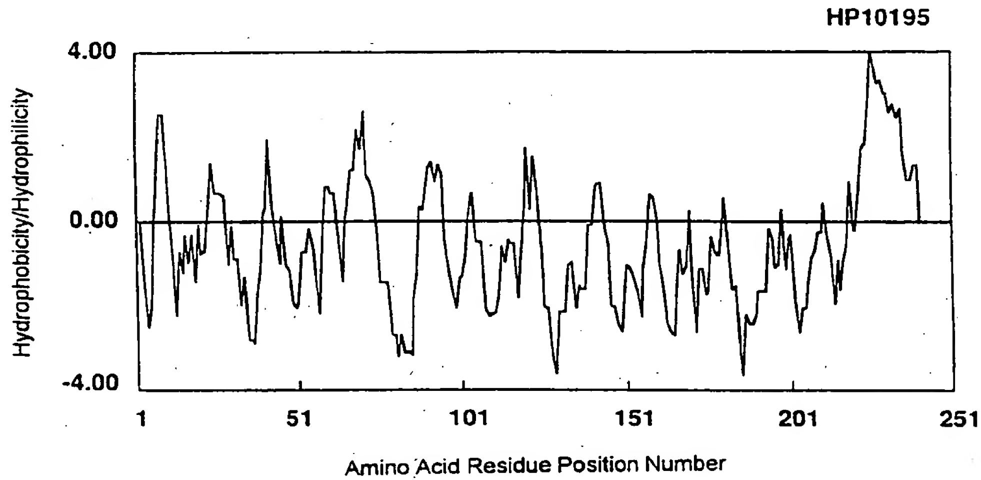
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Fig. 3

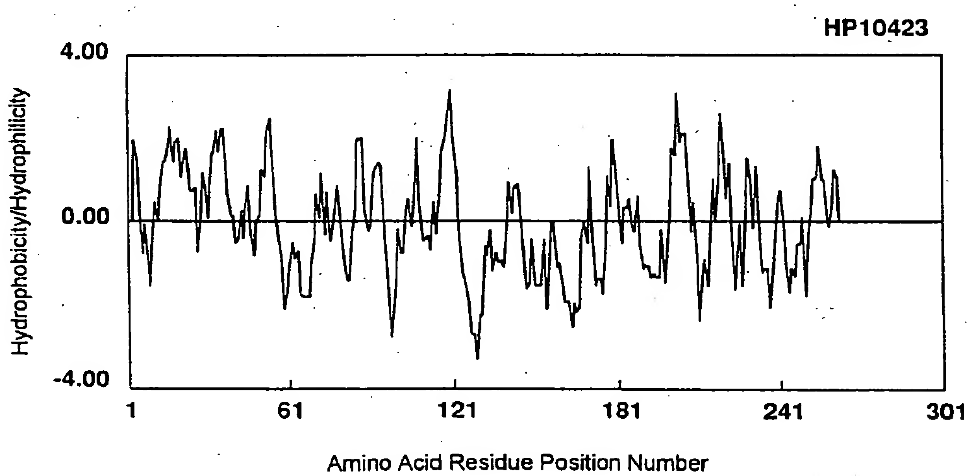
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Fig. 4

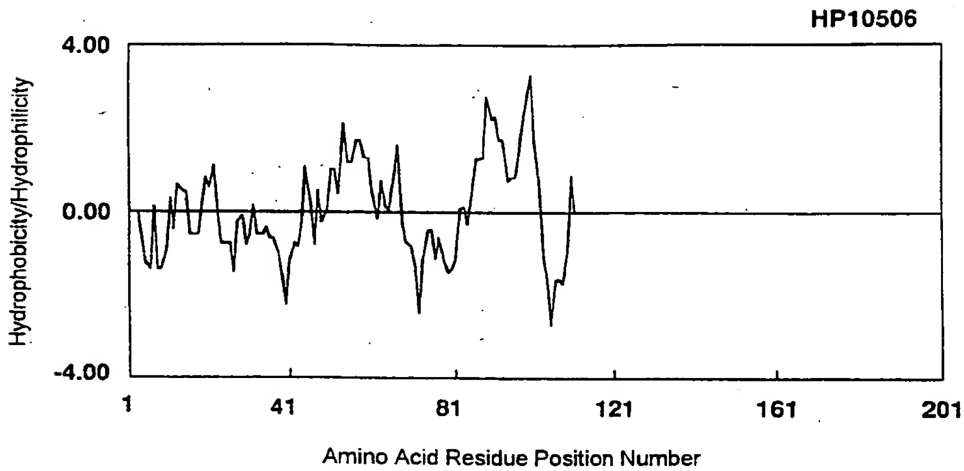
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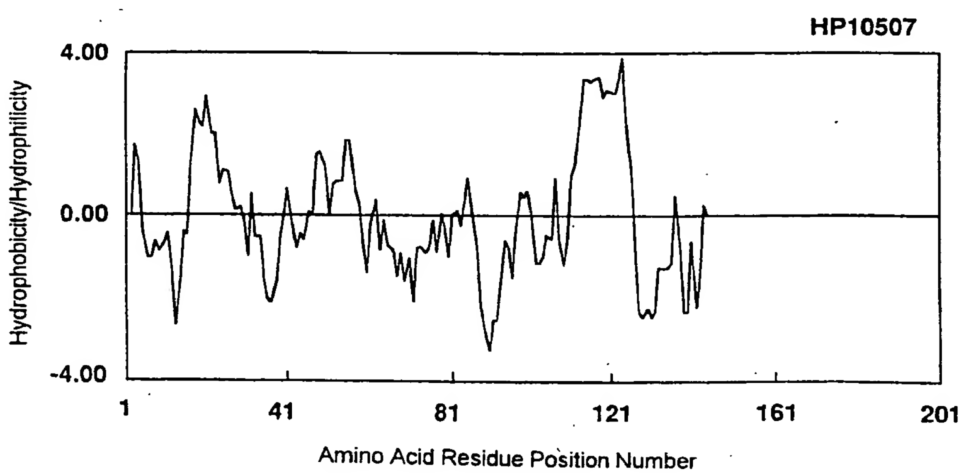
Fig. 5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Hydrophobicity/Hydrophilicity
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161
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Amino Acid Residue Position Number

Fig. 6

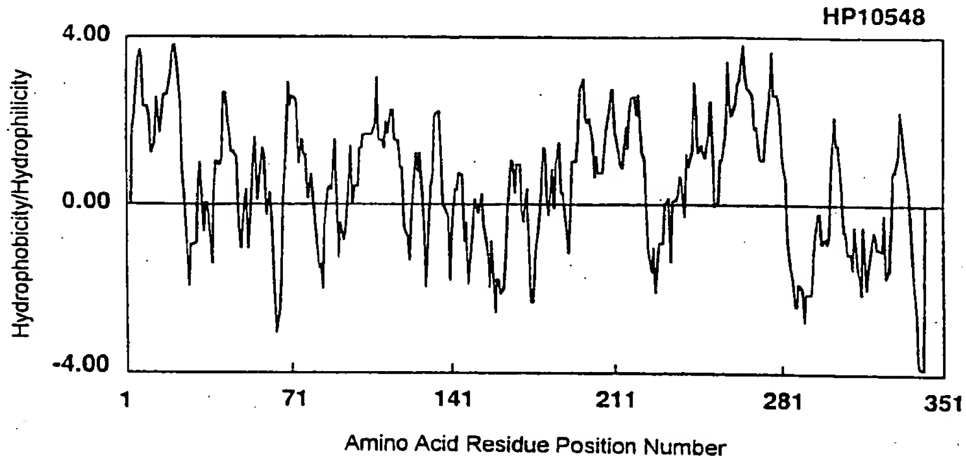
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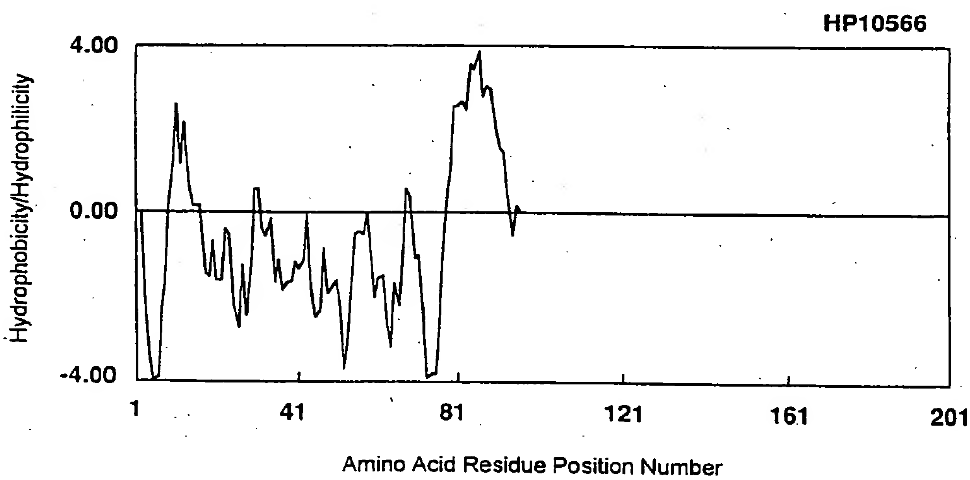
Fig. 7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161
201
Amino Acid Residue Position Number

Fig. 8

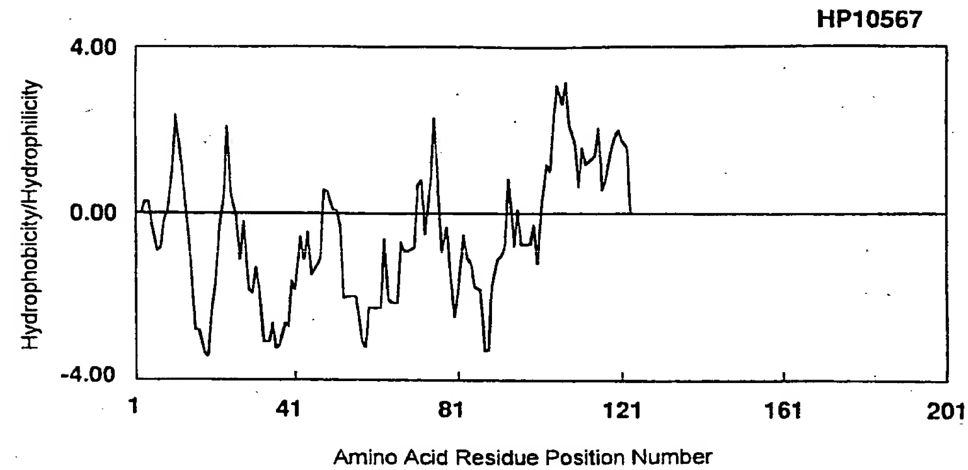


Fig. 9

WO 00/05367

PCT/JP99/03929

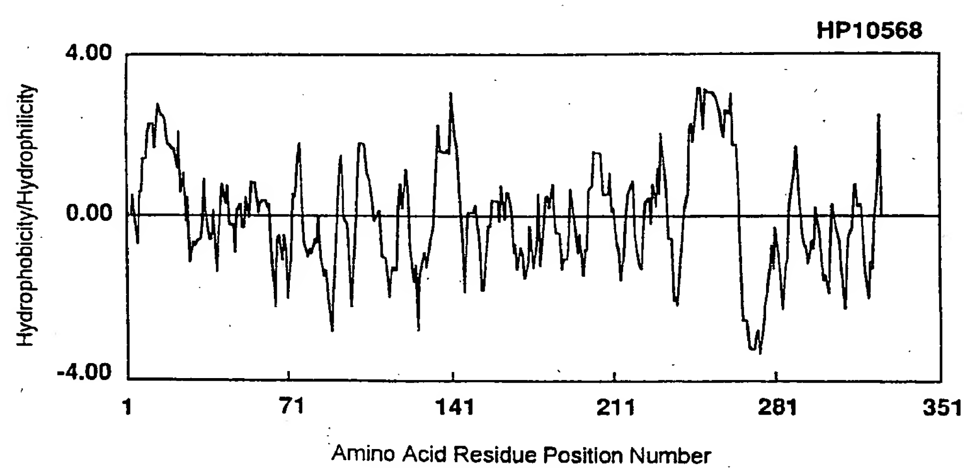
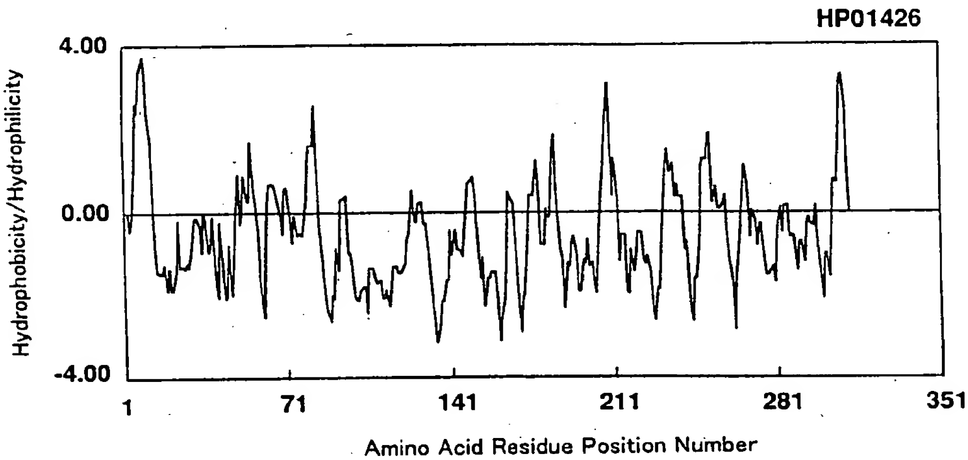


Fig. 10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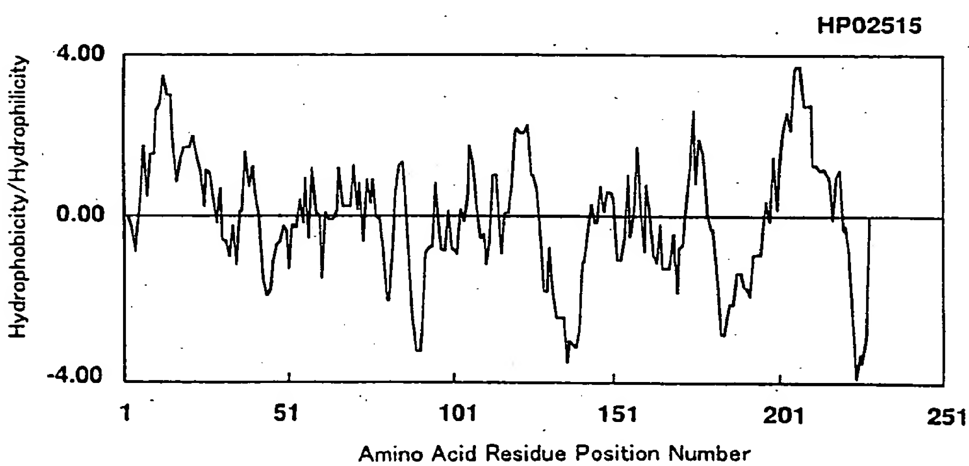
71
141
211
281
351
Amino Acid Residue Position Number

Fig. 11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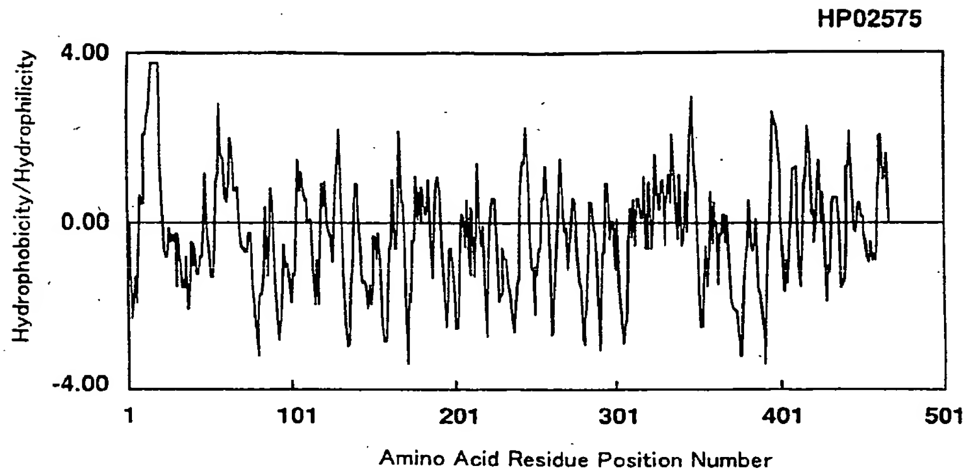
51
101
151
201
251
Amino Acid Residue Position Number

Fig. 12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401
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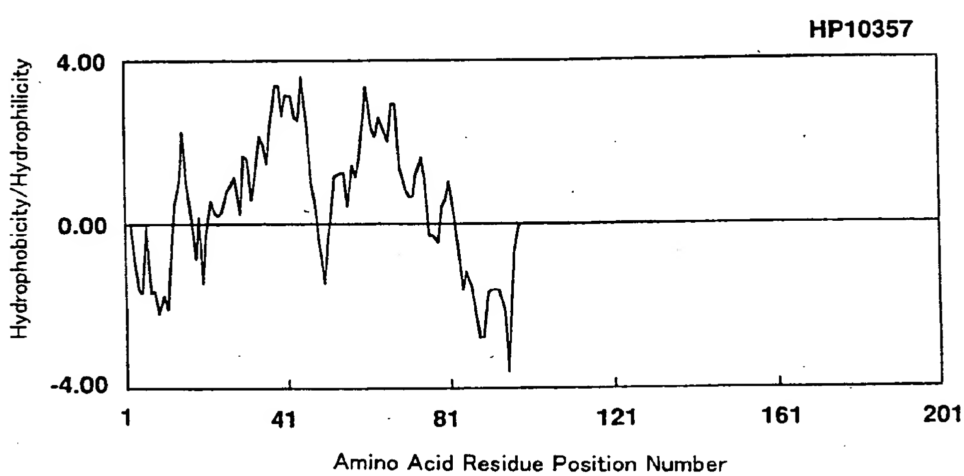
Amino Acid Residue Position Number

Fig. 13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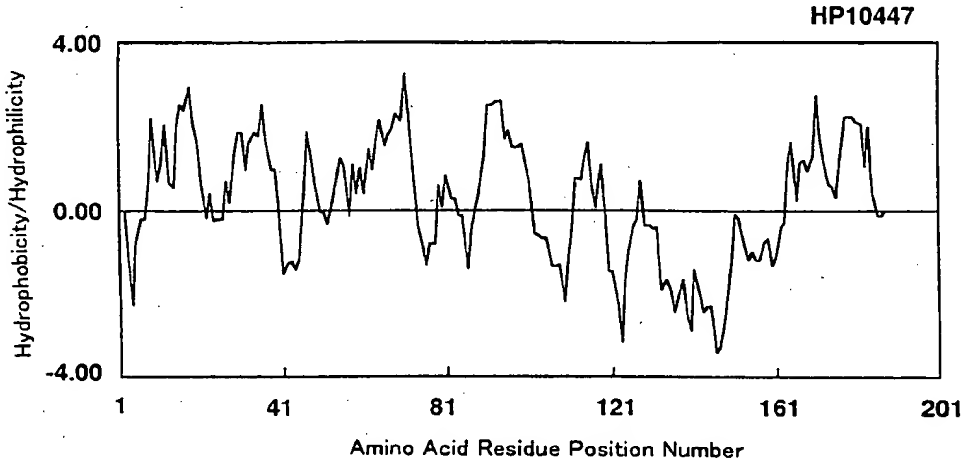
Amino Acid Residue Position Number

Fig. 14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Hydrophobicity/Hydrophilicity
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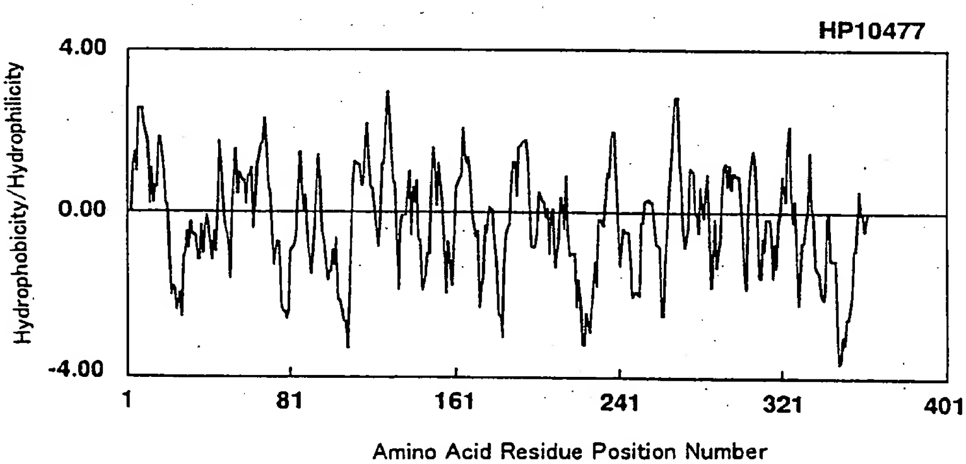
Amino Acid Residue Position Number

Fig. 15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Hydrophobicity/Hydrophilicity
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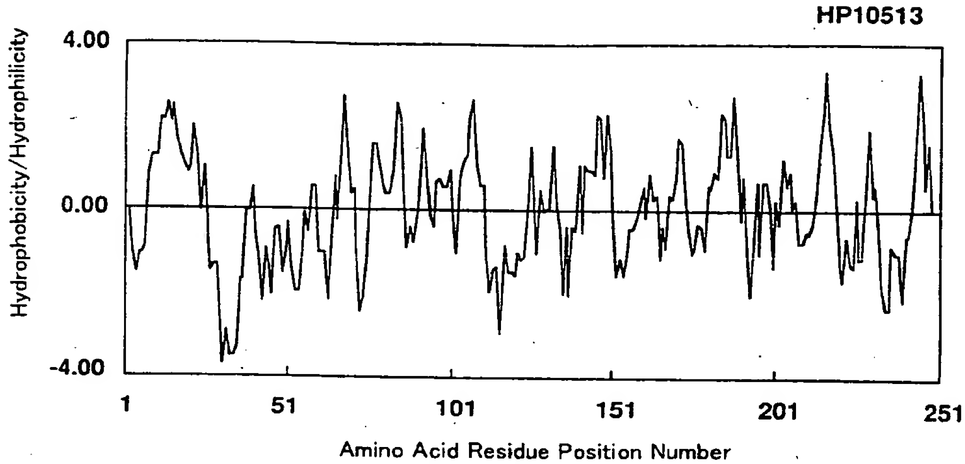
81
161
241
321
401
Amino Acid Residue Position Number

Fig. 16


HP10513
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101
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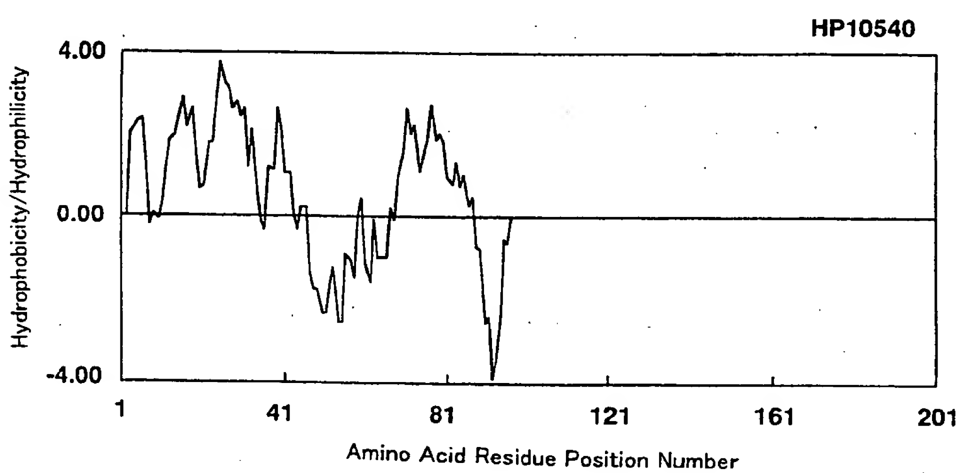
201
251
Amino Acid Residue Position Number

Fig.17


HP10540
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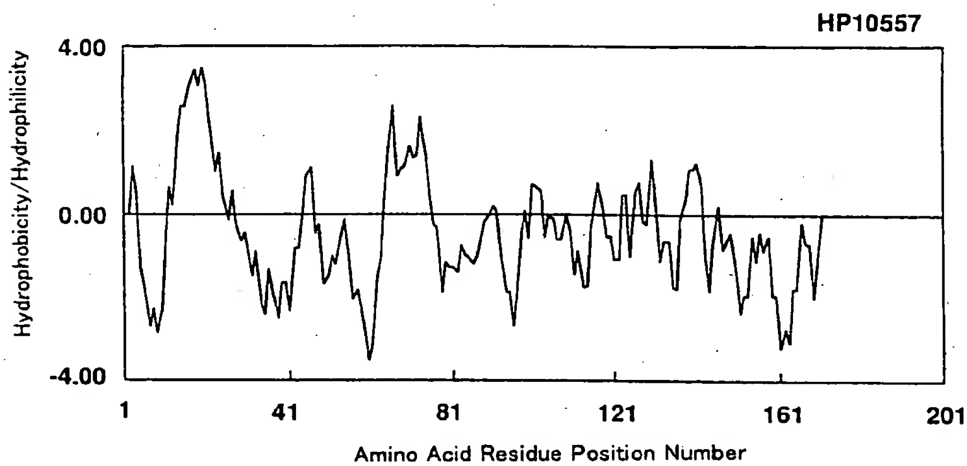
81
121
161
201
Amino Acid Residue Position Number

Fig. 18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Hydrophobicity/Hydrophilicity
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161
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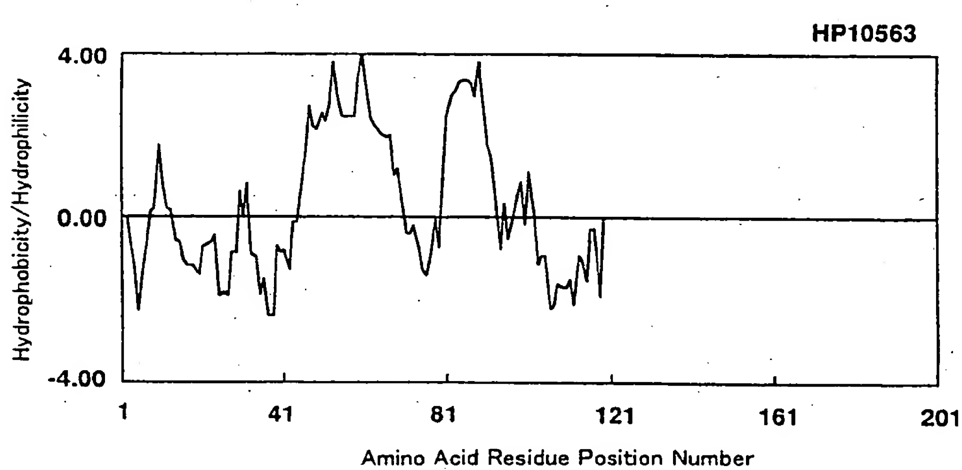
Amino Acid Residue Position Number

Fig. 19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Hydrophobicity/Hydrophilicity
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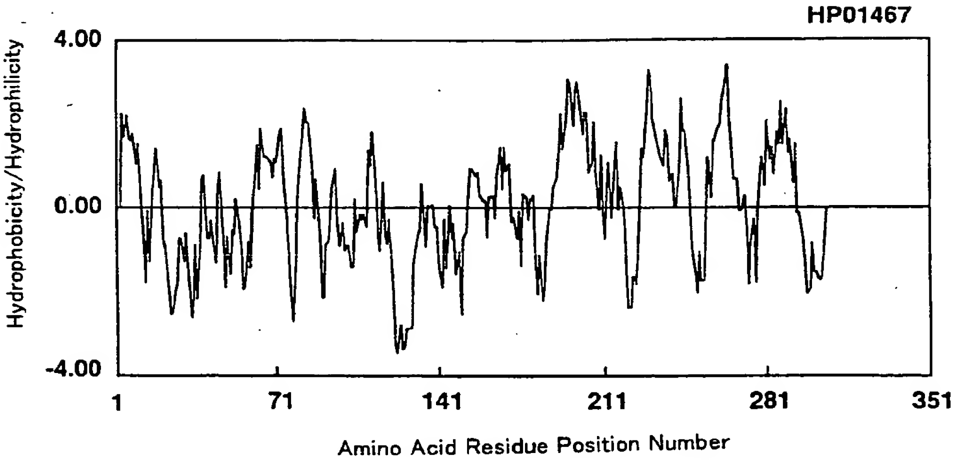
121
161
201
Amino Acid Residue Position Number

Fig. 20


HP01467
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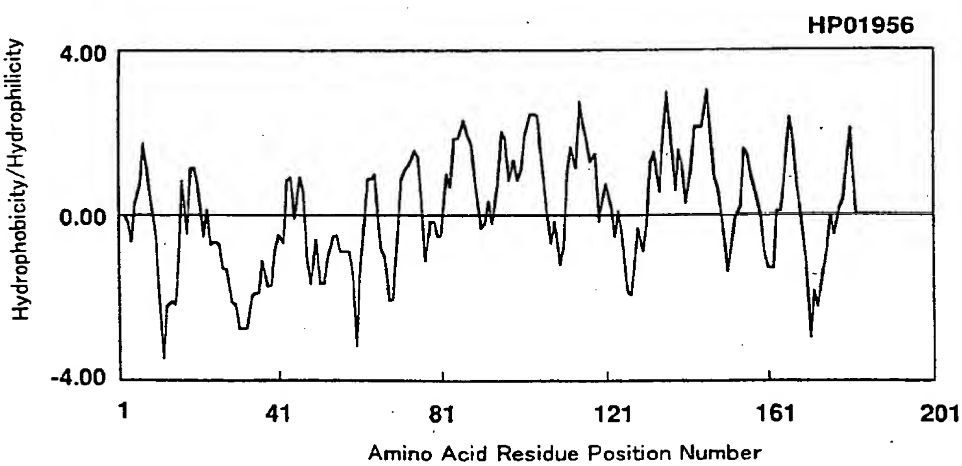
-4.00
Hydrophobicity/Hydrophilicity
1
71
141
211
281
351
Amino Acid Residue Position Number

Fig. 21


HP01956
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0.00
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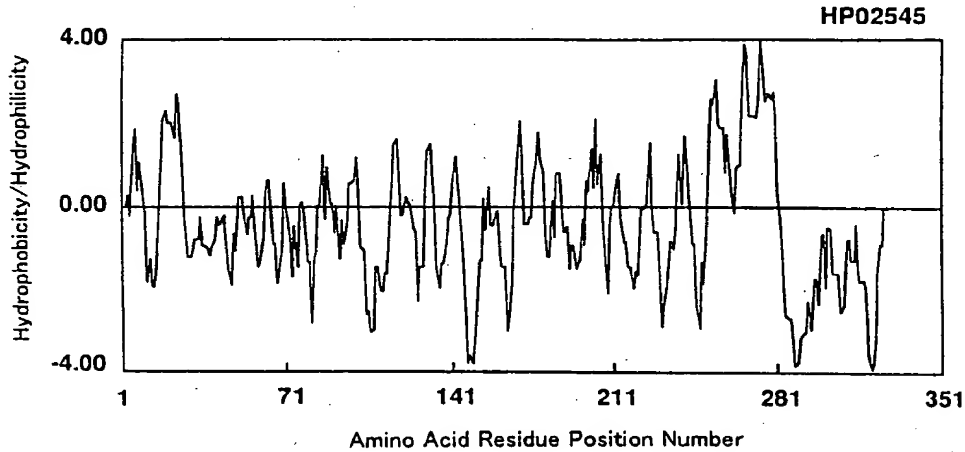
Hydrophobicity/Hydrophilicity
1
41
81
121
161
201
Amino Acid Residue Position Number

Fig.22


HP02545
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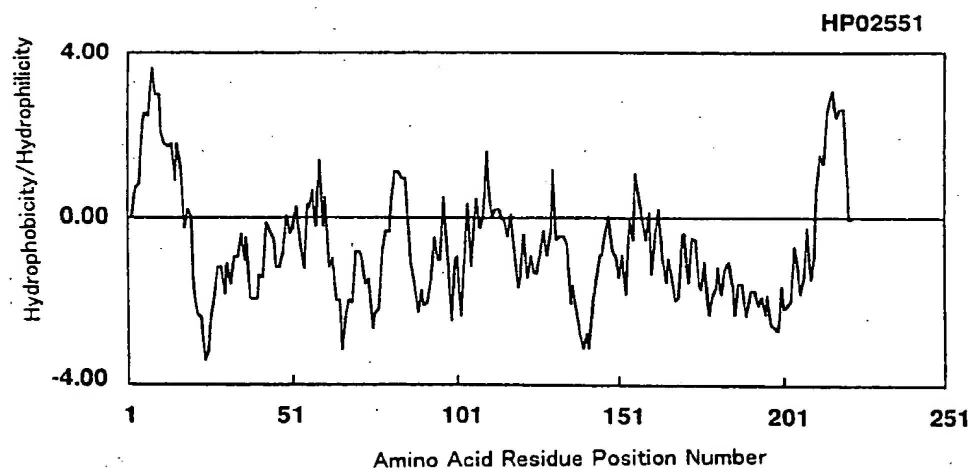
Hydrophobicity/Hydrophilicity
1
71
141
211
281
351
Amino Acid Residue Position Number

Fig. 23


HP02551
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-4.00
Hydrophobicity/Hydrophilicity
1
51
101
151
201
251
Amino Acid Residue Position Number

Fig. 24

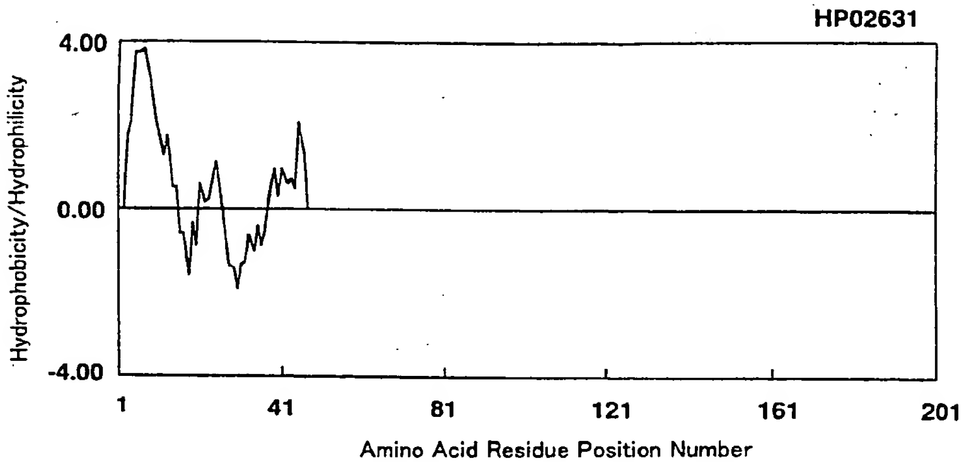
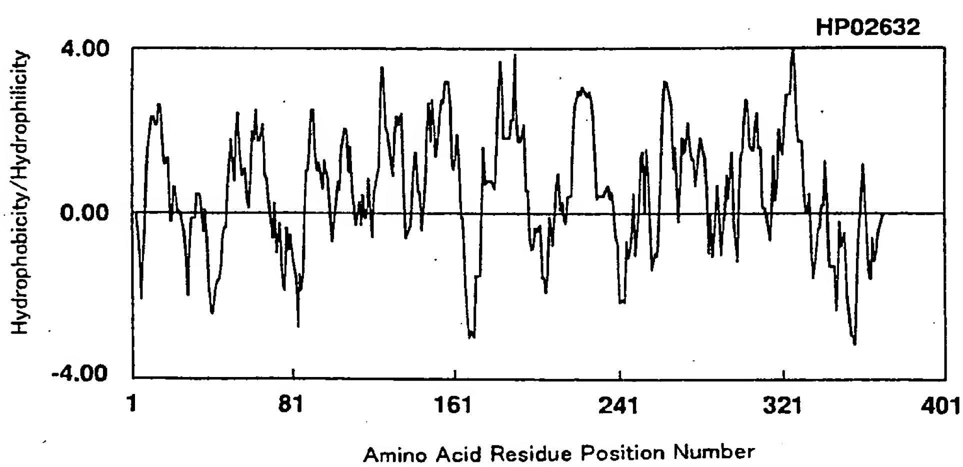

HP02631
4.00
0.00
-4.00
Hydrophobicity/Hydrophilicity
1
41
81
121
161
201
Amino Acid Residue Position Number

Fig. 25


HP02632
4.00
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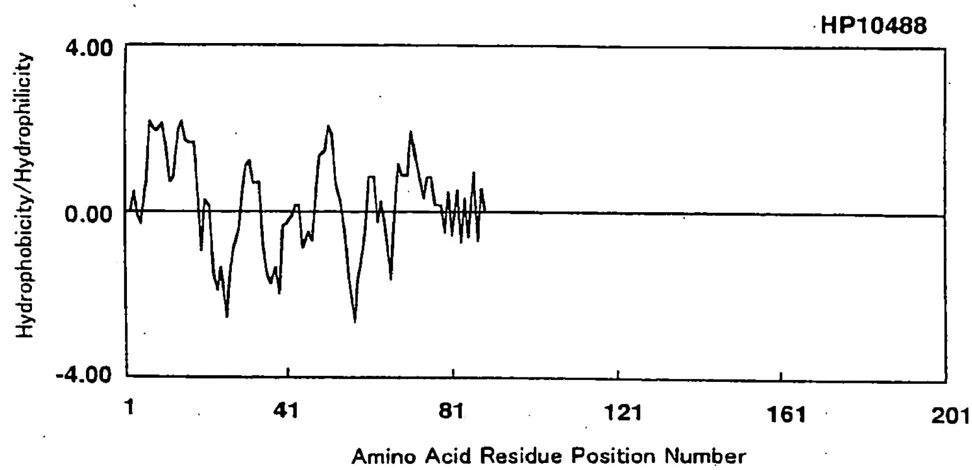
Hydrophobicity/Hydrophilicity
1
81
161
241
321
401
Amino Acid Residue Position Number

Fig. 26


HP10488
Hydrophobicity/Hydrophilicity
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0.00
-4.00
1
41
81
121
161
201
Amino Acid Residue Position Number

Fig.27

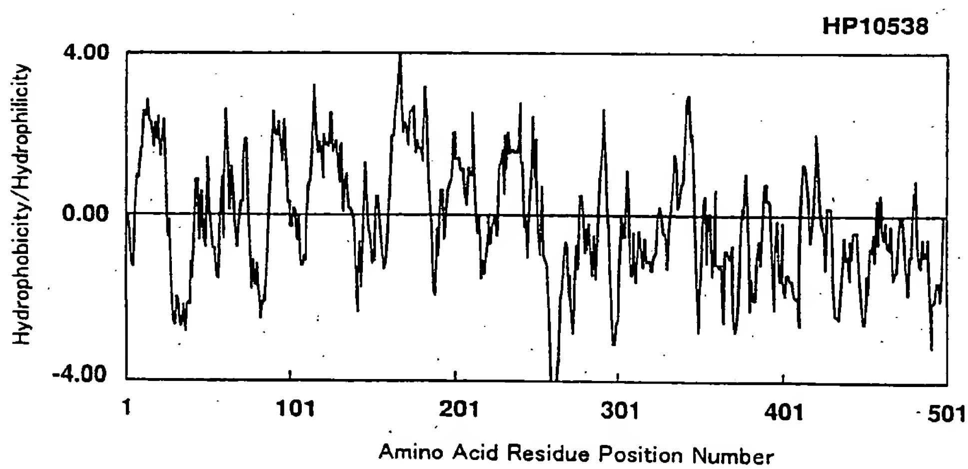
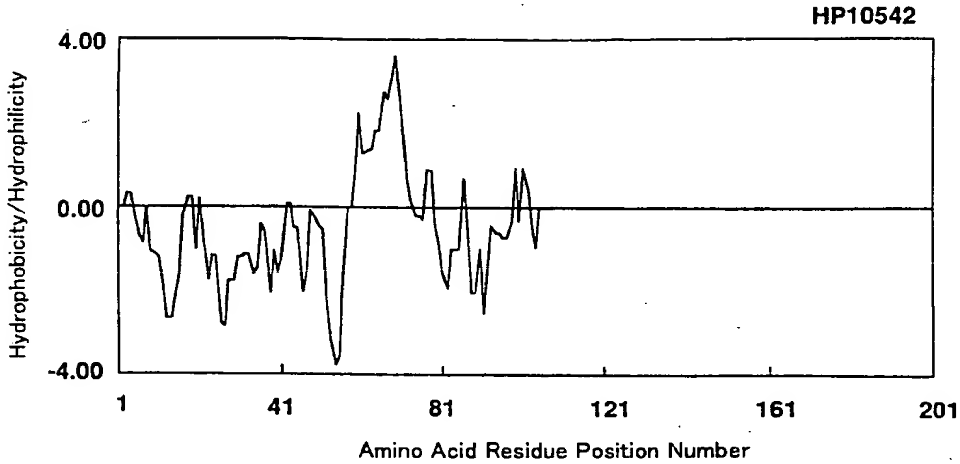

HP10538
Hydrophobicity/Hydrophilicity
4.00
0.00
-4.00
1
101
201
301
401
501
Amino Acid Residue Position Number

Fig. 28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4.00
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Hydrophobicity/Hydrophilicity
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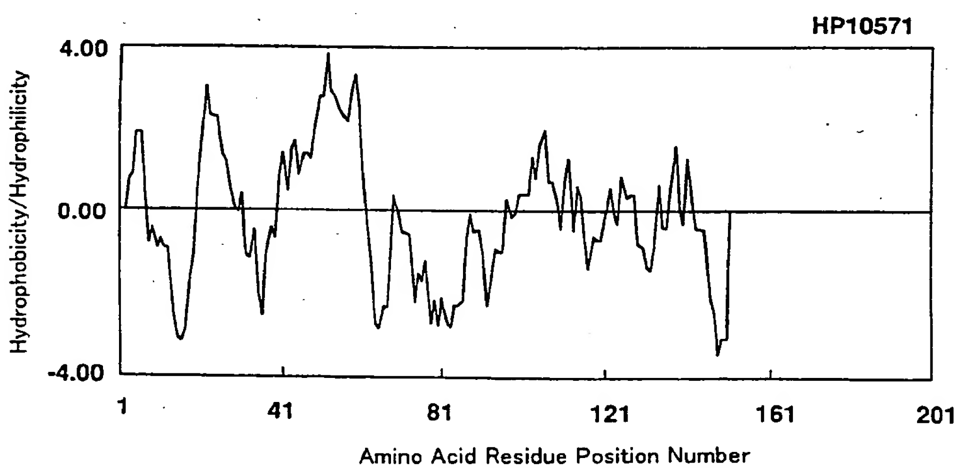
41
81
121
161
201
Amino Acid Residue Position Number

Fig. 29


HP10571
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0.00
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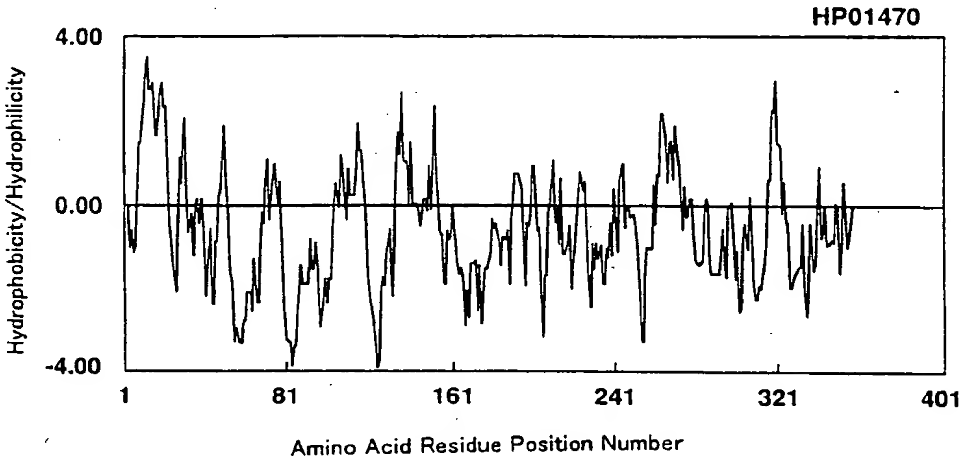
Hydrophobicity/Hydrophilicity
1
41
81
121
161
201
Amino Acid Residue Position Number

Fig. 30


HP01470
4.00
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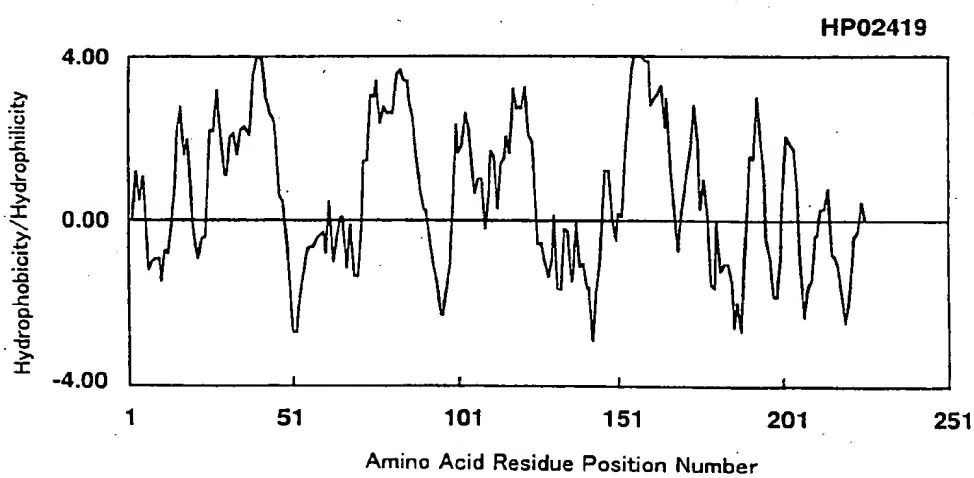
Hydrophobicity/Hydrophilicity
1
81
161
241
321
401
Amino Acid Residue Position Number

Fig. 31


HP02419
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0.00
-4.00
Hydrophobicity/Hydrophilicity
1
51
101
151
201
251
Amino Acid Residue Position Number

Fig.32

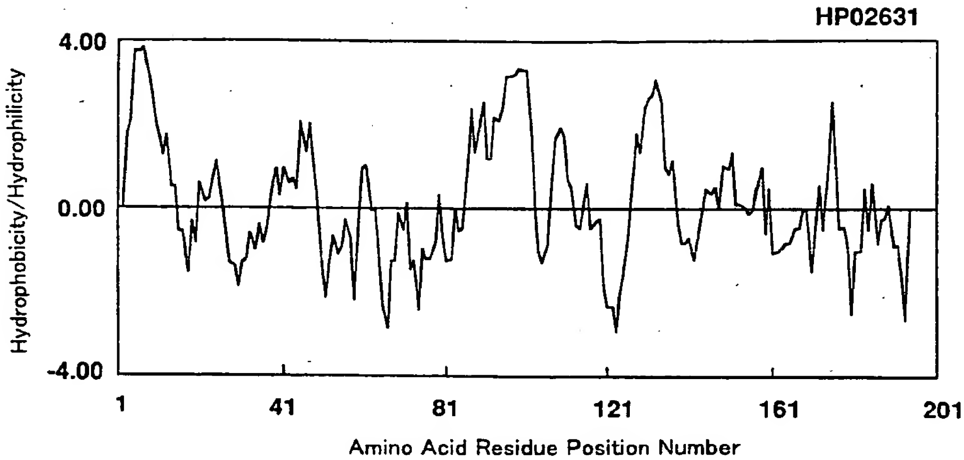
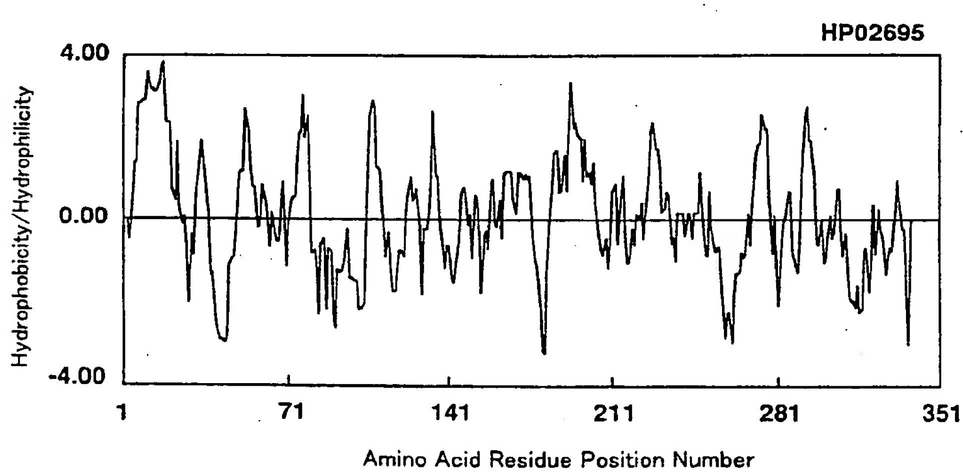

HP02631
4.00
0.00
-4.00
Hydrophobicity/Hydrophilicity
1
41
81
121
161
201
Amino Acid Residue Position Number

Fig. 33


HP02695
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0.00
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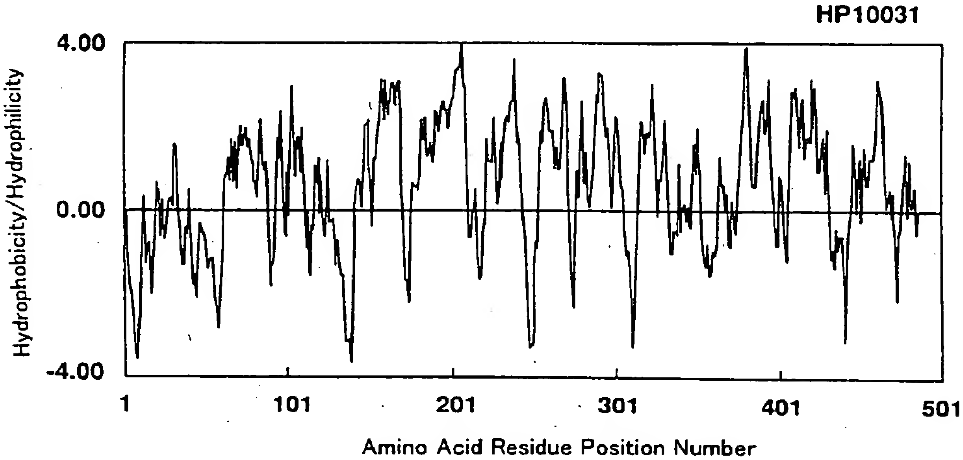
Hydrophobicity/Hydrophilicity
1
71
141
211
281
351
Amino Acid Residue Position Number

Fig. 34


HP10031
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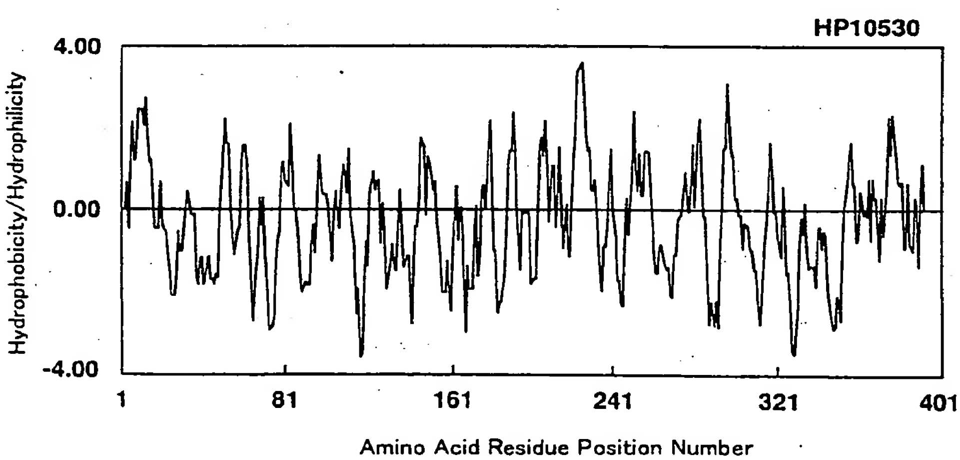
Hydrophobicity/Hydrophilicity
1
101
201
301
401
501
Amino Acid Residue Position Number

Fig. 35


HP10530
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Hydrophobicity/Hydrophilicity
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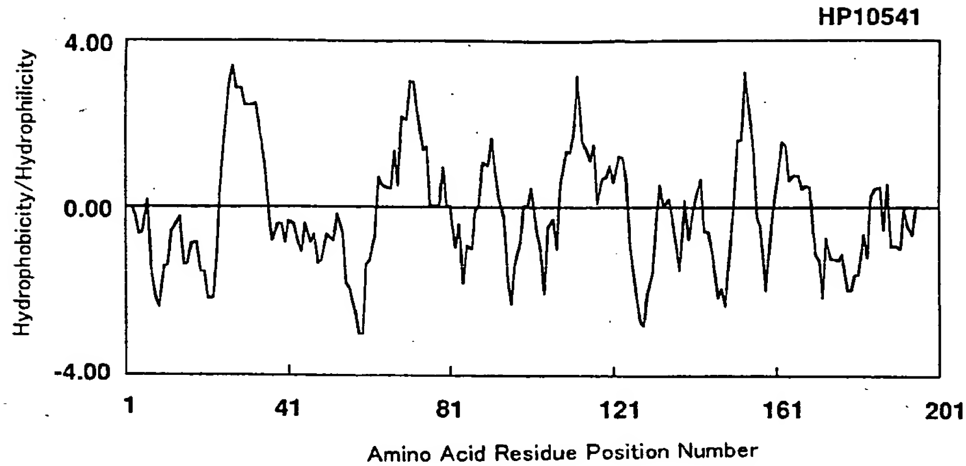
81
161
241
321
401
Amino Acid Residue Position Number

Fig. 36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Hydrophobicity/Hydrophilicity
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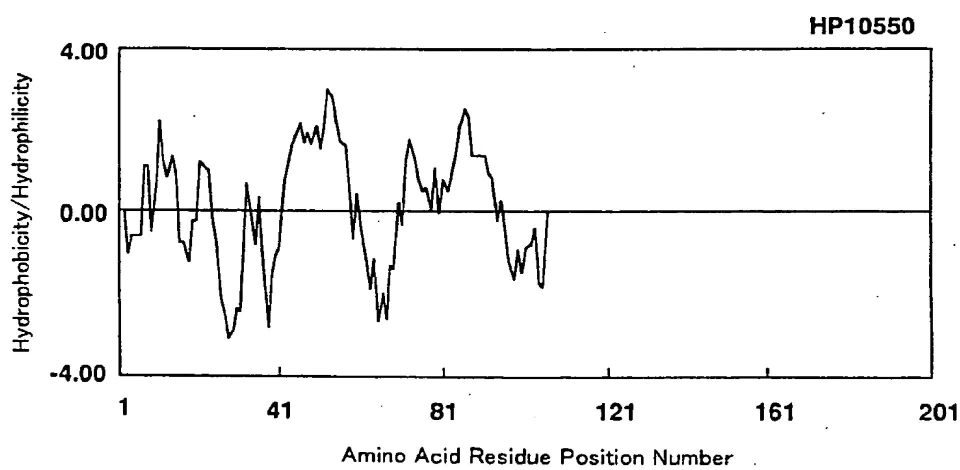
41
81
121
161
201
Amino Acid Residue Position Number

Fig.37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Hydrophobicity/Hydrophilicity
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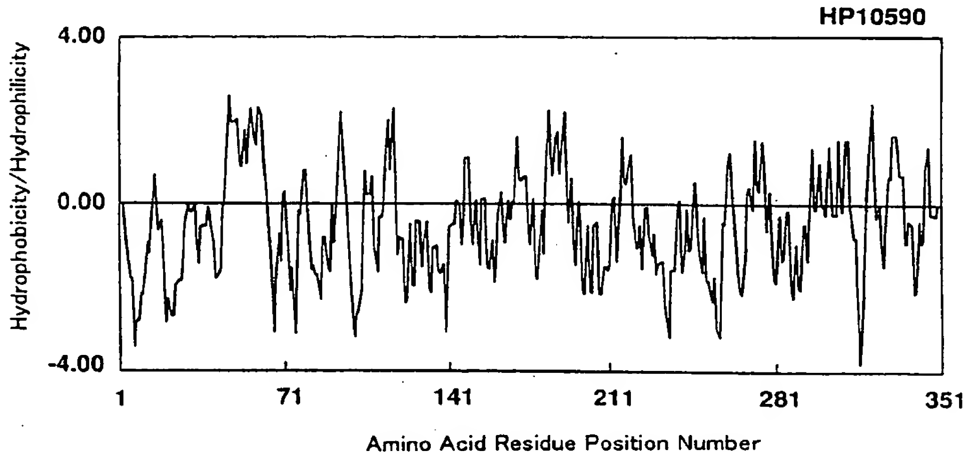
41
81
121
161
201
Amino Acid Residue Position Number

Fig. 38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Hydrophobicity/Hydrophilicity
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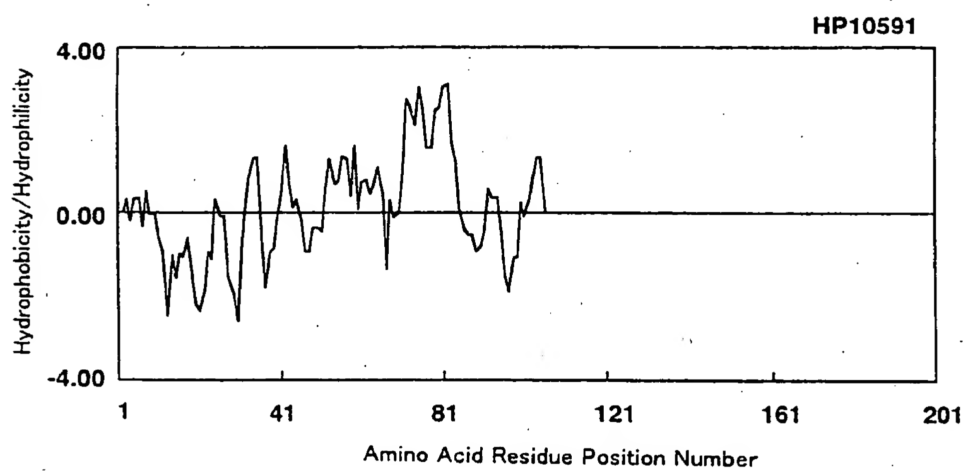
71
141
211
281
351
Amino Acid Residue Position Number

Fig. 39


HP10591
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Hydrophobicity/Hydrophilicity
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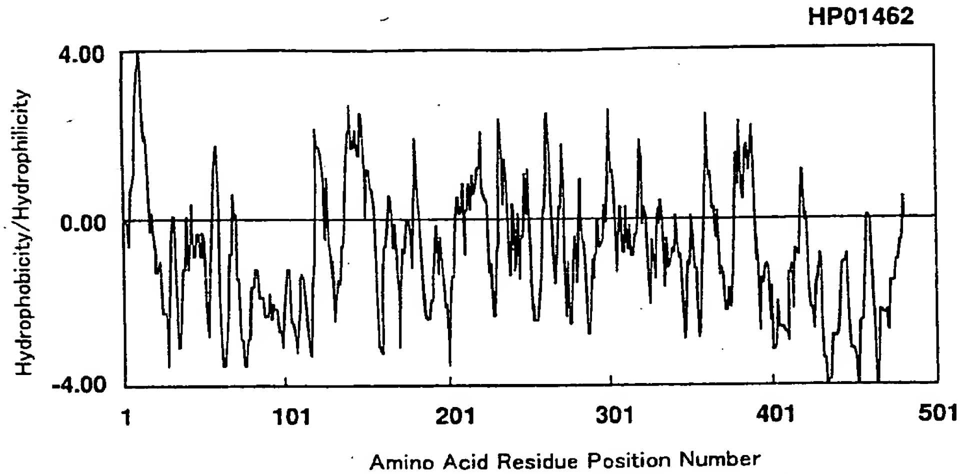
41
81
121
161
201
Amino Acid Residue Position Number

Fig. 40


HP01462
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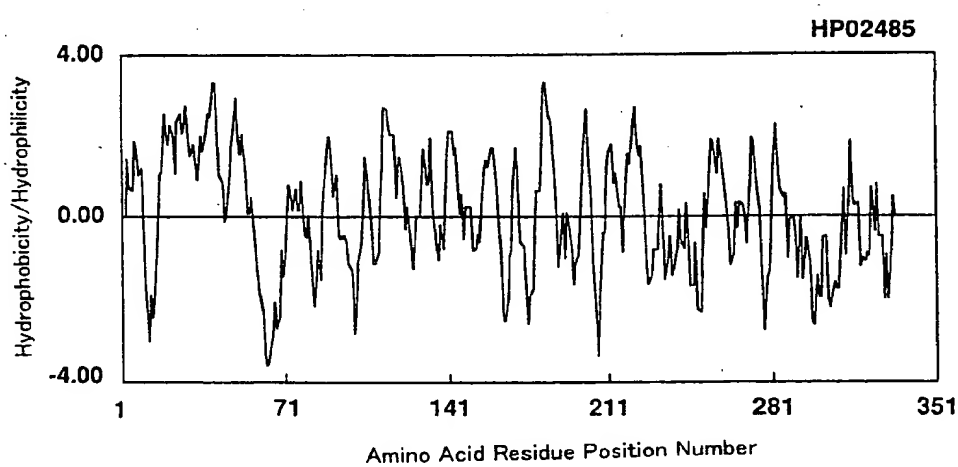
Hydrophobicity/Hydrophilicity
1
101
201
301
401
501
Amino Acid Residue Position Number

Fig. 41


HP02485
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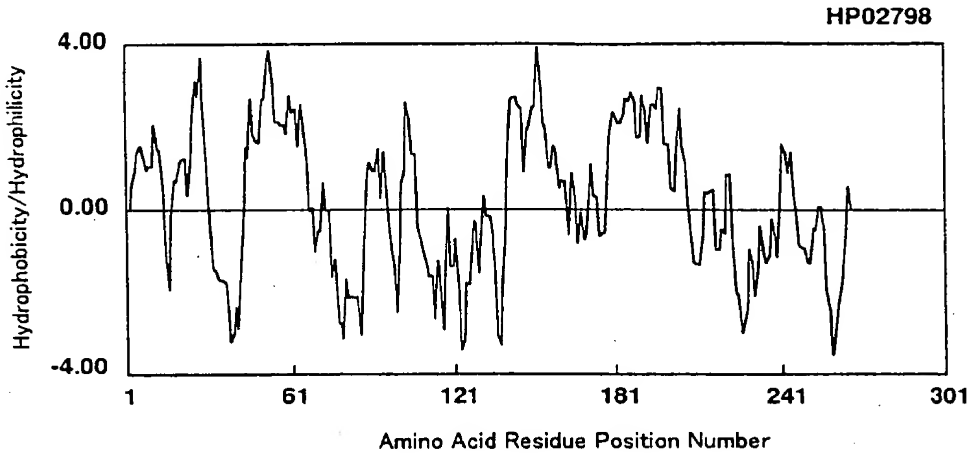
Hydrophobicity/Hydrophilicity
1
71
141
211
281
351
Amino Acid Residue Position Number

Fig.42


HP02798
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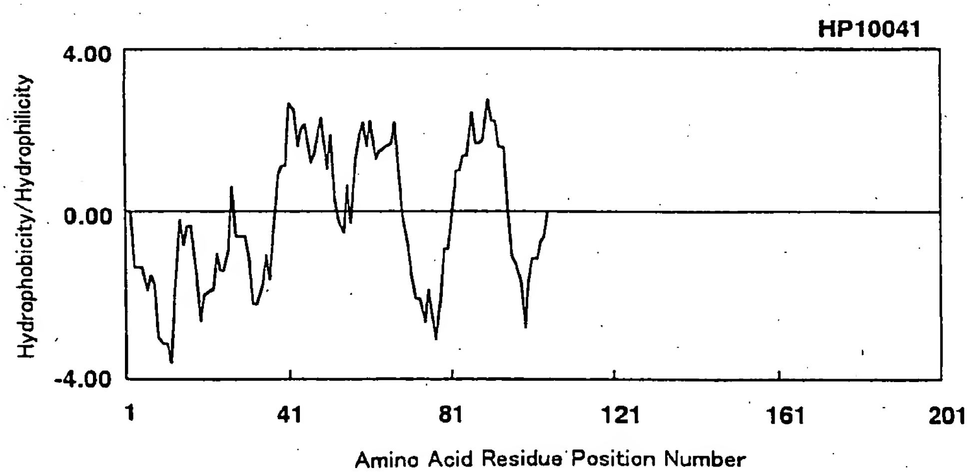
0.00
-4.00
Hydrophobicity/Hydrophilicity
1
61
121
181
241
301
Amino Acid Residue Position Number

Fig. 43


HP10041
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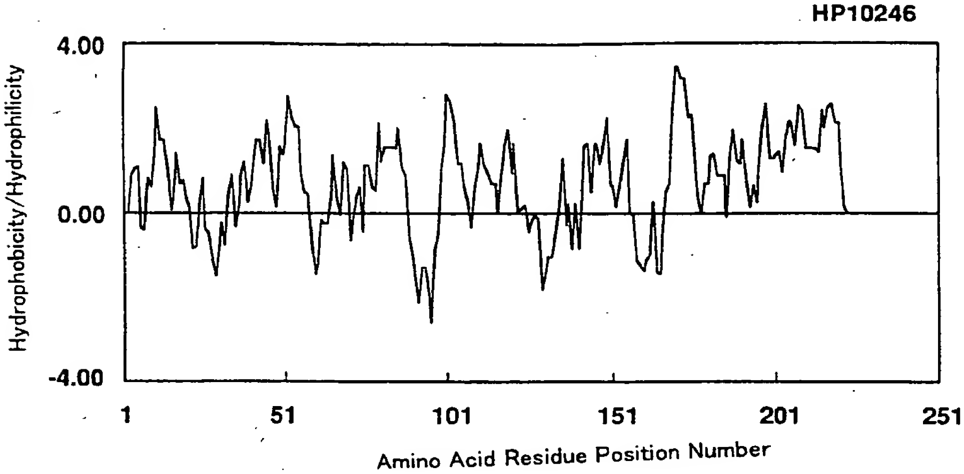
0.00
-4.00
Hydrophobicity/Hydrophilicity
1
41
81
121
161
201
Amino Acid Residue Position Number

Fig. 44


HP10246
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Hydrophobicity/Hydrophilicity
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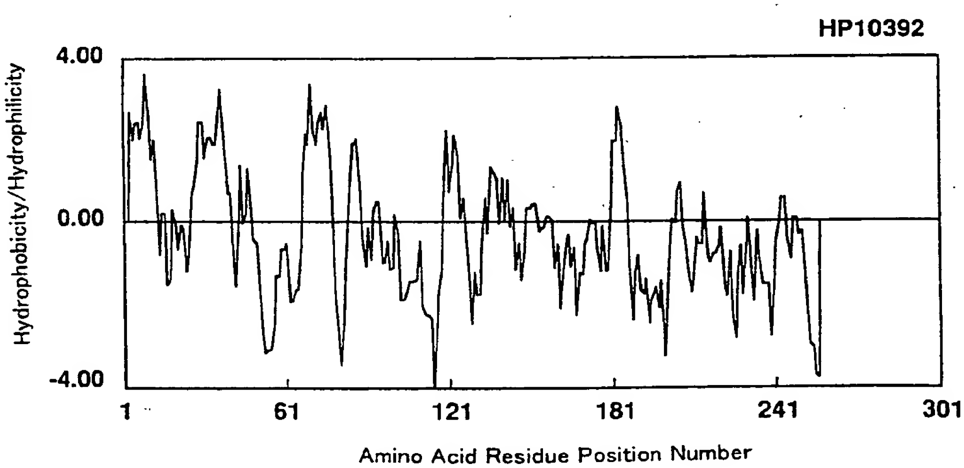
51
101
151
201
251
Amino Acid Residue Position Number

Fig. 45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-4.00
Hydrophobicity/Hydrophilicity
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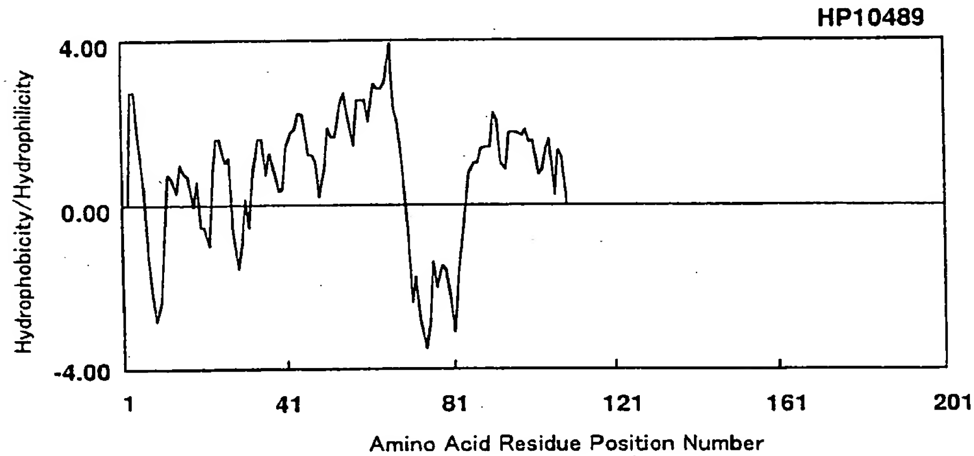
61
121
181
241
301
Amino Acid Residue Position Number

Fig. 46


HP10489
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Hydrophobicity/Hydrophilicity
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41
81
121
161
201
Amino Acid Residue Position Number

Fig.47

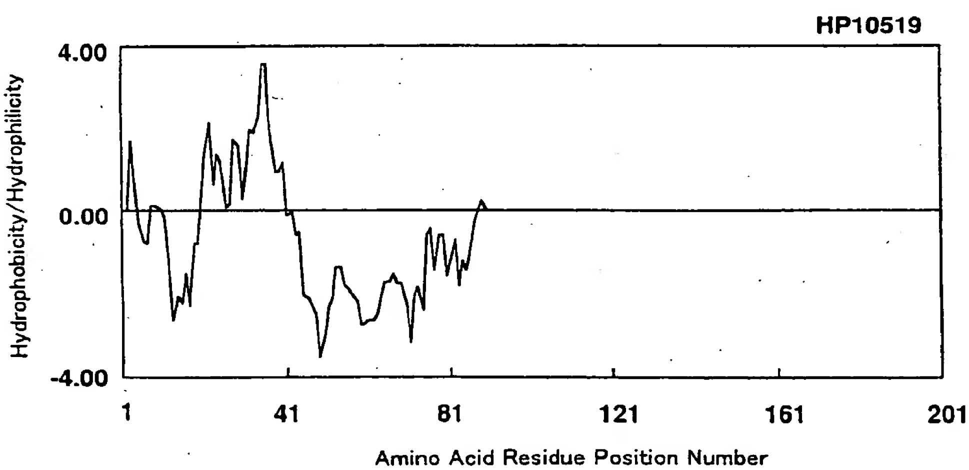
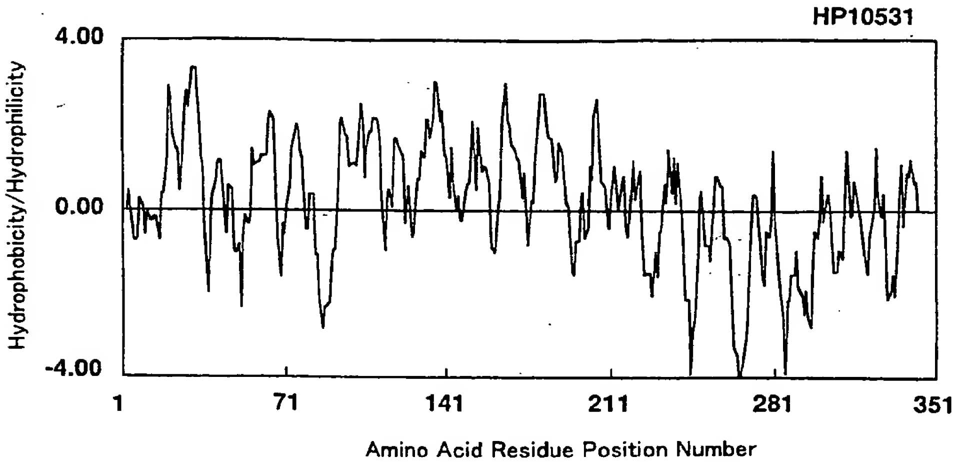

HP10519
4.00
0.00
-4.00
Hydrophobicity/Hydrophilicity
1
41
81
121
161
201
Amino Acid Residue Position Number

Fig. 48


HP10531
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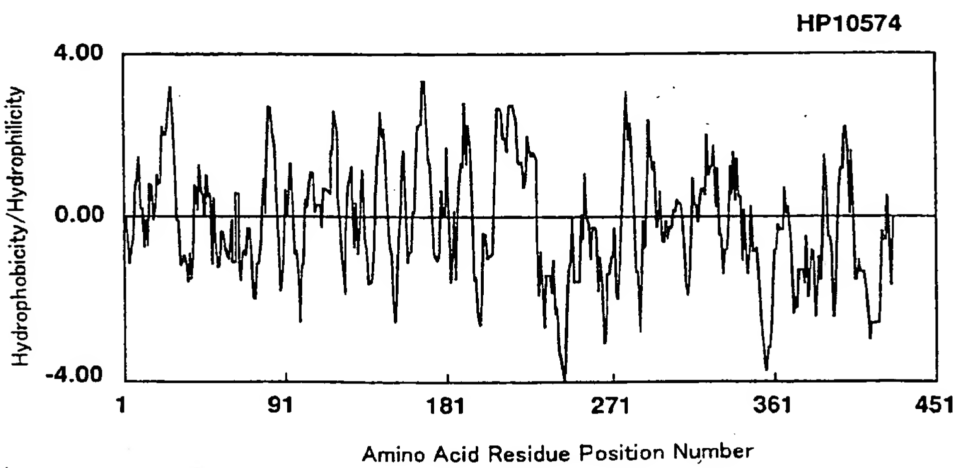
-4.00
Hydrophobicity/Hydrophilicity
1
71
141
211
281
351
Amino Acid Residue Position Number

Fig. 49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Hydrophobicity/Hydrophilicity
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91
181
271
361
451
Amino Acid Residue Position Number

Fig. 50

Sequence listing

<110> Sagami Chemical Research Center; Protegene Inc.

<120> Human Proteins Having Hydrophobic Domains And DNAs Encoding These Proteins

<130> 661102

<150> JP 10-208820
<151> 1998-07-24

<150> JP 10-224105
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<150> JP 10-275505
<151> 1998-09-29

<160> 150

<170> Windows 95 (Word 98)

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<211> 125
<212> PRT
<213> Homo sapiens

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20 25 30
Ala Ala Ala Asp Ala Arg Gly Arg Ala Gly His Arg Ser Ala Ala Ala
35 40 45
Ser Asn Leu Ser Gly Leu Ser Leu Gln Glu Ala Gln Gln Ile Leu Asn
50 55 60
Val Ser Lys Leu Ser Pro Glu Glu Val Gln Lys Asn Tyr Glu His Leu
65 70 75 80
Phe Lys Val Asn Asp Lys Ser Val Gly Gly Ser Phe Tyr Leu Gln Ser
85 90 95
Lys Val Val Arg Ala Lys Glu Arg Leu Asp Glu Glu Leu Lys Ile Gln
100 105 110
Ala Gln Glu Asp Arg Glu Lys Gly Gln Met Pro His Thr
115 120 125

<210> 2
<211> 131
<212> PRT
<213> Homo sapiens

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Gly Leu Met Phe Leu Met Leu Gly Cys Ala Leu Pro Ile Tyr Asn Lys
20 25 30
Tyr Trp Pro Leu Phe Val Leu Phe Phe Tyr Ile Leu Ser Pro Ile Pro
35 40 45
Tyr Cys Ile Ala Arg Arg Leu Val Asp Asp Thr Asp Ala Met Ser Asn
50 55 60
Ala Cys Lys Glu Leu Ala Ile Phe Leu Thr Thr Gly Ile Val Val Ser
65 70 75 80
Ala Phe Gly Leu Pro Ile Val Phe Ala Arg Ala His Leu Ile Glu Trp
85 90 95
Gly Ala Cys Ala Leu Val Leu Thr Gly Asn Thr Val Ile Phe Ala Thr

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            100                 105                 110
Ile Leu Gly Phe Phe Leu Val Phe Gly Ser Asn Asp Asp Phe Ser Trp
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Gln Gln Trp
    130

<210> 3
<211> 242
<212> PRT
<213> Homo sapiens

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Lys Phe Lys Gly Pro Phe Thr Asp Val Val Thr Thr Asn Leu Lys Leu
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Arg Asn Pro Ser Asp Arg Lys Val Cys Phe Lys Val Lys Thr Thr Ala
        35                  40                  45
Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly Ile Ile Asp Pro Gly
    50                  55                  60
Ser Thr Val Thr Val Ser Val Met Leu Gln Pro Phe Asp Tyr Asp Pro
65                  70                  75                  80
Asn Glu Lys Ser Lys His Lys Phe Met Val Gln Thr Ile Phe Ala Pro
                85                  90                  95
Pro Asn Thr Ser Asp Met Glu Ala Val Trp Lys Glu Ala Lys Pro Asp
            100                 105                 110
Glu Leu Met Asp Ser Lys Leu Arg Cys Val Phe Glu Met Pro Asn Glu
        115                 120                 125
Asn Asp Lys Leu Asn Asp Met Glu Pro Ser Lys Ala Val Pro Leu Asn
    130                 135                 140
Ala Ser Lys Gln Asp Gly Pro Met Pro Lys Pro His Ser Val Ser Leu
145                 150                 155                 160
Asn Asp Thr Glu Thr Arg Lys Leu Met Glu Glu Cys Lys Arg Leu Gln
                165                 170                 175
Gly Glu Met Met Lys Leu Ser Glu Glu Asn Arg His Leu Arg Asp Glu
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            180                 185                 190
Gly Leu Arg Leu Arg Lys Val Ala His Ser Asp Lys Pro Gly Ser Thr
        195                 200                 205
Ser Thr Ala Ser Phe Arg Asp Asn Val Thr Ser Pro Leu Pro Ser Leu
    210                 215                 220
Leu Val Val Ile Ala Ala Ile Phe Ile Gly Phe Phe Leu Gly Lys Phe
225                 230                 235                 240
Ile Leu

<210> 4
<211> 264
<212> PRT
<213> Homo sapiens

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            20                  25                  30
Asp Leu Ile Ile Ser Thr Leu Asn Met Ser Lys Ile Gly Tyr Phe Tyr
        35                  40                  45
Thr Asp Cys Leu Val Pro Met Val Gly Asn Asn Pro Tyr Ala Thr Thr
    50                  55                  60
Glu Gly Asn Ser Thr Glu Leu Ser Ile Asn Ala Glu Val Tyr Ser Leu
65                  70                  75                  80
Pro Ser Arg Lys Leu Val Ala Leu Gln Leu Arg Ser Ile Phe Ile Lys
                85                  90                  95
Tyr Lys Ser Lys Pro Phe Cys Glu Lys Leu Leu Ser Trp Val Lys Ser
            100                 105                 110
Ser Gly Cys Ala Arg Val Ile Val Leu Ser Ser Ser His Ser Tyr Gln
        115                 120                 125
Arg Asn Asp Leu Gln Leu Arg Ser Thr Pro Phe Arg Tyr Leu Leu Thr
    130                 135                 140
Pro Ser Met Gln Lys Ser Val Gln Asn Lys Ile Lys Ser Leu Asn Trp
145                 150                 155                 160
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Glu Glu Met Glu Lys Ser Arg Cys Ile Pro Glu Ile Asp Asp Ser Glu
165 170 175
Phe Cys Ile Arg Ile Pro Gly Gly Gly Ile Thr Lys Thr Leu Tyr Asp
180 185 190
Glu Ser Cys Ser Lys Glu Ile Gln Met Ala Val Leu Leu Lys Phe Val
195 200 205
Ser Glu Gly Asp Asn Ile Pro Asp Ala Leu Gly Leu Val Glu Tyr Leu
210 215 220
Asn Glu Trp Leu Gln Ile Leu Lys Pro Leu Ser Asp Asp Pro Thr Val
225 230 235 240
Ser Ala Ser Arg Trp Lys Ile Pro Ser Ser Trp Arg Leu Leu Phe Gly
245 250 255
Ser Gly Leu Pro Pro Ala Leu Phe
260

<210> 5
<211> 112
<212> PRT
<213> Homo sapiens

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20 25 30
Gly Ala Pro Thr Ser Pro Ala Glu His Arg Leu Leu Lys Thr Cys Trp
35 40 45
Ser Cys Arg Val Leu Ser Gly Leu Gly Leu Met Gly Ala Gly Gly Tyr
50 55 60
Val Tyr Trp Val Ala Arg Lys Pro Met Lys Met Gly Tyr Pro Pro Ser
65 70 75 80
Pro Trp Thr Ile Thr Gln Met Val Ile Gly Leu Ser Ile Ala Thr Trp
85 90 95
Gly Ile Val Val Met Ala Asp Pro Lys Gly Lys Ala Tyr Arg Val Val
100 105 110

<210> 6
<211> 146
<212> PRT
<213> Homo sapiens

<400> 6
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Cys Trp Leu Leu Cys Ala Phe Thr Leu Lys Leu Cys Gln Ala Glu Ala
20 25 30
Pro Val Gln Glu Glu Lys Leu Ser Ala Ser Thr Ser Asn Leu Pro Cys
35 40 45
Trp Leu Val Glu Glu Phe Val Val Ala Glu Glu Cys Ser Pro Cys Ser
50 55 60
Asn Phe Arg Ala Lys Thr Thr Pro Glu Cys Gly Pro Thr Gly Tyr Val
65 70 75 80
Glu Lys Ile Thr Cys Ser Ser Ser Lys Arg Asn Glu Phe Lys Ser Cys
85 90 95
Arg Ser Ala Leu Met Glu Gln Arg Leu Phe Trp Lys Phe Glu Gly Ala
100 105 110
Val Val Cys Val Ala Leu Ile Phe Ala Cys Leu Val Ile Ile Arg Gln
115 120 125
Arg Gln Leu Asp Arg Lys Ala Leu Glu Lys Val Arg Lys Gln Ile Glu
130 135 140
Ser Ile
145

<210> 7
<211> 344
<212> PRT
<213> Homo sapiens

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            20                  25                  30
Leu Ala Arg Gly Gly Ala Gln Ile Phe Ser Cys Ile Ile Pro Glu Cys
        35                  40                  45
Leu Gln Arg Ala Val His Gly Leu Leu His Tyr Leu Phe His Thr Arg
    50                  55                  60
Asn His Thr Phe Ile Val Leu His Leu Val Leu Gln Gly Met Val Tyr
65                  70                  75                  80
Thr Glu Tyr Thr Trp Glu Val Phe Gly Tyr Cys Gln Glu Leu Glu Leu
                85                  90                  95
Ser Leu His Tyr Leu Leu Leu Pro Tyr Leu Leu Leu Gly Val Asn Leu
            100                 105                 110
Phe Phe Phe Thr Leu Thr Cys Gly Thr Asn Pro Gly Ile Ile Thr Lys
        115                 120                 125
Ala Asn Glu Leu Leu Phe Leu His Val Tyr Glu Phe Asp Glu Val Met
    130                 135                 140
Phe Pro Lys Asn Val Arg Cys Ser Thr Cys Asp Leu Arg Lys Pro Ala
145                 150                 155                 160
Arg Ser Lys His Cys Ser Val Cys Asn Trp Cys Val His Arg Phe Asp
                165                 170                 175
His His Cys Val Trp Val Asn Asn Cys Ile Gly Ala Trp Asn Ile Arg
            180                 185                 190
Tyr Phe Leu Ile Tyr Val Leu Thr Leu Thr Ala Ser Ala Ala Thr Val
        195                 200                 205
Ala Ile Val Ser Thr Thr Phe Leu Val His Leu Val Val Met Ser Asp
    210                 215                 220
Leu Tyr Gln Glu Thr Tyr Ile Asp Asp Leu Gly His Leu His Val Met
225                 230                 235                 240
Asp Thr Val Phe Leu Ile Gln Tyr Leu Phe Leu Thr Phe Pro Arg Ile
                245                 250                 255
Val Phe Met Leu Gly Phe Val Val Val Leu Ser Phe Leu Leu Gly Gly
            260                 265                 270
Tyr Leu Leu Phe Val Leu Tyr Leu Ala Ala Thr Asn Gln Thr Thr Asn
        275                 280                 285
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Glu Trp Tyr Arg Gly Asp Trp Ala Trp Cys Gln Arg Cys Pro Leu Val
    290                 295                 300
Ala Trp Pro Pro Ser Ala Glu Pro Gln Val His Arg Asn Ile His Ser
305                 310                 315                 320
His Gly Leu Arg Ser Asn Leu Gln Glu Ile Phe Leu Pro Ala Phe Pro
                325                 330                 335
Cys His Glu Arg Lys Lys Gln Glu
            340
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<210> 8
<211> 97
<212> PRT
<213> Homo sapiens

<400> 8

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Met Thr Lys Lys Lys Arg Glu Asn Leu Gly Val Ala Leu Glu Ile Asp
1               5                   10                  15
Gly Leu Glu Glu Lys Leu Ser Gln Cys Arg Arg Asp Leu Glu Ala Val
            20                  25                  30
Asn Ser Arg Leu His Ser Arg Glu Leu Ser Pro Glu Ala Arg Arg Ser
        35                  40                  45
Leu Glu Lys Glu Lys Asn Ser Leu Met Asn Lys Ala Ser Asn Tyr Glu
    50                  55                  60
Lys Glu Leu Lys Phe Leu Arg Gln Glu Asn Arg Lys Asn Met Leu Leu
65                  70                  75                  80
Ser Val Ala Ile Phe Ile Leu Leu Thr Leu Val Tyr Ala Tyr Trp Thr
                85                  90                  95
Met
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<210> 9
<211> 124
<212> PRT
<213> Homo sapiens

<400> 9

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Met Ala Thr Ser Ser Met Ser Lys Gly Cys Phe Val Phe Lys Pro Asn
 1               5                  10                  15
Ser Lys Lys Arg Lys Ile Ser Leu Pro Ile Glu Asp Tyr Phe Asn Lys
            20                  25                  30
Gly Lys Asn Glu Pro Glu Asp Ser Lys Leu Arg Phe Glu Thr Tyr Gln
        35                  40                  45
Leu Ile Trp Gln Gln Met Lys Ser Glu Asn Glu Arg Leu Gln Glu Glu
    50                  55                  60
Leu Asn Lys Asn Leu Phe Asp Asn Leu Ile Glu Phe Leu Gln Lys Ser
65                  70                  75                  80
His Ser Gly Phe Gln Lys Asn Ser Arg Asp Leu Gly Gly Gln Ile Lys
                85                  90                  95
Leu Arg Glu Ile Pro Thr Ala Ala Leu Val Leu Gly Ile Tyr Ala Tyr
            100                 105                 110
Val Cys Ser Cys Met His Leu Cys Val Phe Arg Phe
        115                 120
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<210> 10
<211> 327
<212> PRT
<213> Homo sapiens

<400> 10

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Met Ala Glu Leu Pro Gly Pro Phe Leu Cys Gly Ala Leu Leu Gly Phe
 1               5                  10                  15
Leu Cys Leu Ser Gly Leu Ala Val Glu Val Lys Val Pro Thr Glu Pro
            20                  25                  30
Leu Ser Thr Pro Leu Gly Lys Thr Ala Glu Leu Thr Cys Thr Tyr Ser
        35                  40                  45
Thr Ser Val Gly Asp Ser Phe Ala Leu Glu Trp Ser Phe Val Gln Pro
    50                  55                  60
Gly Lys Pro Ile Ser Glu Ser His Pro Ile Leu Tyr Phe Thr Asn Gly
65                  70                  75                  80
His Leu Tyr Pro Thr Gly Ser Lys Ser Lys Arg Val Ser Leu Leu Gln
                85                  90                  95
```



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Asn Pro Pro Thr Val Gly Val Ala Thr Leu Lys Leu Thr Asp Val His
            100                 105                 110
Pro Ser Asp Thr Gly Thr Tyr Leu Cys Gln Val Asn Asn Pro Pro Asp
        115                 120                 125
Phe Tyr Thr Asn Gly Leu Gly Leu Ile Asn Leu Thr Val Leu Val Pro
    130                 135                 140
Pro Ser Asn Pro Leu Cys Ser Gln Ser Gly Gln Thr Ser Val Gly Gly
145                 150                 155                 160
Ser Thr Ala Leu Arg Cys Ser Ser Ser Glu Gly Ala Pro Lys Pro Val
                165                 170                 175
Tyr Asn Trp Val Arg Leu Gly Thr Phe Pro Thr Pro Ser Pro Gly Ser
            180                 185                 190
Met Val Gln Asp Glu Val Ser Gly Gln Leu Ile Leu Thr Asn Leu Ser
        195                 200                 205
Leu Thr Ser Ser Gly Thr Tyr Arg Cys Val Ala Thr Asn Gln Met Gly
    210                 215                 220
Ser Ala Ser Cys Glu Leu Thr Leu Ser Val Thr Glu Pro Ser Gln Gly
225                 230                 235                 240
Arg Val Ala Gly Ala Leu Ile Gly Val Leu Leu Gly Val Leu Leu Leu
                245                 250                 255
Ser Val Ala Ala Phe Cys Leu Val Arg Phe Gln Lys Glu Arg Gly Lys
            260                 265                 270
Lys Pro Lys Glu Thr Tyr Gly Gly Ser Asp Leu Arg Glu Asp Ala Ile
        275                 280                 285
Ala Pro Gly Ile Ser Glu His Thr Cys Met Arg Ala Asp Ser Ser Lys
    290                 295                 300
Gly Phe Leu Glu Arg Pro Ser Ser Ala Ser Thr Val Thr Thr Thr Lys
305                 310                 315                 320
Ser Lys Leu Pro Met Val Val
                325
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<210> 11
<211> 375
<212> DNA
<213> Homo sapiens

<400> 11
atggccaagt acctggccca gatcattgtg atgggcgtgc aggtggtggg cagggccttt 60
gcacgggcct tgcggcagga gtttgcagcc agccgggccg cagctgatgc ccgaggacgc 120
gctggacacc ggtctgcagc cgcttccaac ctctccggcc tcagcctcca ggaggcacag 180
cagattctca acgtgtccaa gctgagccct gaggaggtcc agaagaacta tgaacactta 240
tttaaggtga atgataaatc cgtgggtggc tccttctacc tgcagtcaaa ggtggtccgc 300
gcaaaggagc gcctggatga ggaactcaaa atccaggccc aggaggacag agaaaaaggg 360
cagatgcccc atacg 375

<210> 12
<211> 393
<212> DNA
<213> Homo sapiens

<400> 12
atggcaggca tcaaagcttt gattagtttg tcctttggag gagcaatcgg actgatgttt 60
ttgatgcttg gatgtgccct tccaatatac aacaaatact ggcccctctt tgttctattt 120
ttttacatcc tttcacctat tccatactgc atagcaagaa gattagtgga tgatacagat 180
gctatgagta acgcttgtaa ggaacttgcc atctttctta caacgggcat tgtcgtgtca 240
gcttttggac tccctattgt atttgccaga gcacatctga ttgagtgggg agcttgtgca 300
cttgttctca caggaaacac agtcatcttt gcaactatac taggcttttt cttggtcttt 360
ggaagcaatg acgacttcag ctggcagcag tgg 393

<210> 13
<211> 726
<212> DNA
<213> Homo sapiens

<400> 13
atggcgaagc acgagcagat cctggtcctc gatccgccca cagacctcaa attcaaaggc 60
cccttcacag atgtagtcac tacaaatctt aaattgcgaa atccatcgga tagaaaagtg 120
tgtttcaaag tgaagactac agcacctcgc cggtactgtg tgaggcccaa cagtggaatt 180
attgacccag ggtcaactgt gactgtttca gtaatgctac agccctttga ctatgatccg 240
aatgaaaaga gtaaacacaa gtttatggta cagacaattt ttgctccacc aaacacttca 300

gatatggaag ctgtgtggaa agaggcaaaa cctgatgaat taatggattc caaattgaga 360
tgcgtatttg aaatgcccaa tgaaaatgat aaattgaatg atatggaacc tagcaaagct 420
gttccactga atgcatctaa gcaagatgga cctatgccaa aaccacacag tgtttcactt 480
aatgataccg aaacaaggaa actaatggaa gagtgtaaaa gacttcaggg agaaatgatg 540
aagctatcag aagaaaatcg gcacctgaga gatgaaggtt taaggctcag aaaggtagca 600
cattcggata aacctggatc aacctcaact gcatccttca gagataatgt caccagtcct 660
cttccttcac ttcttgttgt aattgcagcc attttcattg gattctttct agggaaattc 720
atcttg 726

<210> 14
<211> 792
<212> DNA
<213> Homo sapiens

<400> 14
atgttcgttc cctgcgggga gtcggccccc gaccttgccg gcttcaccct cctaatgcca 60
gcagtatctg ttggaaatgt tggccagctt gcaatggatc tgattatttc tacactgaat 120
atgtctaaga ttggttactt ctataccgat tgtcttgtgc caatggttgg aaacaatcca 180
tatgcgacca cagaaggaaa ttcaacagaa cttagcataa atgctgaagt gtattcattg 240
ccttcaagaa agctggtggc tctacagtta agatccattt ttattaagta taaatcaaag 300
ccattctgtg aaaaactgct ttcctgggtg aaaagcagtg gctgtgccag agtcattgtt 360
ctttcgagca gtcattcata tcagcgtaat gatctgcagc ttcgtagtac tcccttccgg 420
tacctactta caccttccat gcaaaaaagt gttcaaaata aaataaagag ccttaactgg 480
gaagaaatgg aaaaaagccg gtgcattcct gaaatagatg attccgagtt ttgtatccgc 540
attccgggag gaggtatcac aaaaacactc tatgatgaaa gctgttctaa agaaatccaa 600
atggcagttc tgctgaaatt tgtttcagaa ggggacaaca tcccagatgc attaggtctt 660
gttgagtatc ttaatgagtg gcttcagata ctcaaaccac ttagcgatga ccccacagta 720
tctgcctcac ggtggaaaat accaagttct tggagattac tctttggcag tggtcttccc 780
cctgcacttt tc 792

<210> 15
<211> 336
<212> DNA
<213> Homo sapiens

<400> 15

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gccgcgcccg ccaaacctgc gcccccagct acacccggag cgccgacctc cccagcagaa 120

caccgcctgt tgaagacctg ctggagctgt cgcgtgcttt ctgggttggg gctgatgggg 180

gcgggcgggt acgtgtactg ggtggcacgg aagcccatga agatgggata ccccccgagt 240

ccatggacca ttacgcagat ggtcatcggc ctcagcattg ccacctgggg tatcgttgtc 300

atggcagacc ccaaagggaa ggcctaccgc gttgtt 336

<210> 16

<211> 438

<212> DNA

<213> Homo sapiens

<400> 16

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tgtgctttca ccttaaagct ctgccaagca gaggctcccg tgcaggaaga gaagctgtca 120

gcaagcacct caaatttgcc atgctggctg gtggaagagt ttgtggtagc agaagagtgc 180

tctccatgct ctaatttccg ggctaaaact acccctgagt gtggtcccac aggatatgta 240

gagaaaatca catgcagctc atctaagaga aatgagttca aaagctgccg ctcagctttg 300

atggaacaac gcttattttg gaagttcgaa ggggctgtcg tgtgtgtggc cctgatcttc 360

gcttgtcttg tcatcattcg tcagcgacaa ttggacagaa aggctctgga aaaggtccgg 420

aagcaaatcg agtccata 438

<210> 17

<211> 1032

<212> DNA

<213> Homo sapiens

<400> 17

atggactttc tggtcctctt cttgttctac ctggcttcgg tgctgatggg tcttgttctt 60

atctgcgtct gctcgaaaac ccatagcttg aaaggcctgg ccaggggagg agcacagata 120

ttttcctgta taattccaga atgtcttcag agagccgtgc atggattgct tcattacctt 180

ttccatacga gaaaccacac cttcattgtc ctgcacctgg tcttgcaagg gatggtttat 240

actgagtaca cctgggaagt atttggctac tgtcaggagc tggagttgtc cttgcattac 300

cttcttctgc cctatctgct gctaggtgta aacctgtttt ttttcaccct gacttgtgga 360

accaatcctg gcattataac aaaagcaaat gaattattat ttcttcatgt ttatgaattt 420

gatgaagtga tgtttccaaa gaacgtgagg tgctctactt gtgatttaag gaaaccagct 480

cgatccaagc actgcagtgt gtgtaactgg tgtgtgcacc gtttcgacca tcactgtgtt 540

tgggtgaaca actgcatcgg ggcctggaac atcaggtact tcctcatcta cgtcttgacc 600

ttgacggcct cggctgccac cgtcgccatt gtgagcacca cttttctggt ccacttggtg 660

gtgatgtcag atttatacca ggagacttac atcgatgacc ttggacacct ccatgttatg 720

gacacggtct ttcttattca gtacctgttc ctgacttttc cacggattgt cttcatgctg 780

ggctttgtcg tggttctgag cttcctcctg ggtggctacc tgttgtttgt cctgtatctg 840

gcggccacca accagactac taacgagtgg tacagaggtg actgggcctg gtgccagcgt 900

tgtccccttg tggcctggcc tccgtcagca gagccccaag tccaccggaa cattcactcc 960

catgggcttc ggagcaacct tcaagagatc tttctacctg cctttccatg tcatgagagg 1020

aagaaacaag aa 1032

<210> 18

<211> 291

<212> DNA

<213> Homo sapiens

<400> 18

atgactaaaa agaagcggga gaatctgggc gtcgctctag agatcgatgg gctagaggag 60

aagctgtccc agtgtcggag agacctggag gccgtgaact ccagactcca cagccgggag 120

ctgagcccag aggccaggag gtccctggag aaggagaaaa acagcctaat gaacaaagcc 180

tccaactacg agaaggaact gaagtttctt cggcaagaga accggaagaa catgctgctc 240

tctgtggcca tctttatcct cctgacgctc gtctatgcct actggaccat g 291

<210> 19

<211> 372

<212> DNA

<213> Homo sapiens

<400> 19

atggctacgt cctcgatgtc taagggttgc tttgttttta agccaaactc caaaaagaga 60

aagatctctc tgccaataga ggactatttt aacaaaggga aaaatgagcc tgaggacagt 120

aagcttcgat tcgaaactta tcagttgata tggcagcaga tgaaatctga aaatgagcga 180

ctacaagagg aattaaataa aaacttgttt gacaatctga ttgaatttct gcaaaaatca 240

cattctggat tccagaagaa ttcaagagac ttgggcggtc aaataaaact cagagaaatt 300
ccaactgctg ctcttgttct tggtatatat gcgtatgttt gttcatgcat gcatctctgt 360
gtatttcgtt tt 372

<210> 20
<211> 981
<212> DNA
<213> Homo sapiens

<400> 20
atggccgagc tcccggggcc ctttctctgc ggggccctgc taggcttcct gtgcctgagt 60
gggctggccg tggaggtgaa ggtacccaca gagccgctga gcacgcccct ggggaagaca 120
gccgagctga cctgcaccta cagcacgtcg gtgggagaca gcttcgccct ggagtggagc 180
tttgtgcagc ctgggaaacc catctctgag tcccatccaa tcctgtactt caccaatggc 240
catctgtatc caactggttc taagtcaaag cgggtcagcc tgcttcagaa cccccccaca 300
gtgggggtgg ccacactgaa actgactgac gtccacccct cagatactgg aacctacctc 360
tgccaagtca acaacccacc agatttctac accaatgggt tggggctaat caaccttact 420
gtgctggttc cccccagtaa tcccttatgc agtcagagtg gacaaacctc tgtgggaggc 480
tctactgcac tgagatgcag ctcttccgag gggctcccta agccagtgta caactgggtg 540
cgtcttggaa ctttcctac accttctcct ggcagcatgg ttcaagatga ggtgtctggc 600
cagctcattc tcaccaacct ctccctgacc tcctcgggca cctaccgctg tgtggccacc 660
aaccagatgg gcagtgcatc ctgtgagctg accctctctg tgaccgaacc ctcccaaggc 720
cgagtggccg gagctctgat tggggtgctc ctgggcgtgc tgttgctgtc agttgctgcg 780
ttctgcctgg tcaggttcca gaaagagagg gggaagaagc ccaaggagac atatgggggt 840
agtgaccttc gggaggatgc catcgctcct gggatctctg agcacacttg tatgagggct 900
gattctagca aggggttcct ggaaagaccc tcgtctgcca gcaccgtgac gaccaccaag 960
tccaagctcc ctatggtcgt g 981

<210> 21
<211> 510
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (66)...(443)

<400> 21
acgcttgatc cccggccgcg gggccaggaa gtcggagttt gagcccccgga ggcagagcgg 60
ctgcc atg gcc aag tac ctg gcc cag atc att gtg atg ggc gtg cag gtg 110
Met Ala Lys Tyr Leu Ala Gln Ile Ile Val Met Gly Val Gln Val
1 5 10 15
gtg ggc agg gcc ttt gca cgg gcc ttg cgg cag gag ttt gca gcc agc 158
Val Gly Arg Ala Phe Ala Arg Ala Leu Arg Gln Glu Phe Ala Ala Ser
20 25 30
cgg gcc gca gct gat gcc cga gga cgc gct gga cac cgg tct gca gcc 206
Arg Ala Ala Ala Asp Ala Arg Gly Arg Ala Gly His Arg Ser Ala Ala
35 40 45
gct tcc aac ctc tcc ggc ctc agc ctc cag gag gca cag cag att ctc 254
Ala Ser Asn Leu Ser Gly Leu Ser Leu Gln Glu Ala Gln Gln Ile Leu
50 55 60
aac gtg tcc aag ctg agc cct gag gag gtc cag aag aac tat gaa cac 302
Asn Val Ser Lys Leu Ser Pro Glu Glu Val Gln Lys Asn Tyr Glu His
65 70 75
tta ttt aag gtg aat gat aaa tcc gtg ggt ggc tcc ttc tac ctg cag 350
Leu Phe Lys Val Asn Asp Lys Ser Val Gly Gly Ser Phe Tyr Leu Gln
80 85 90 95
tca aag gtg gtc cgc gca aag gag cgc ctg gat gag gaa ctc aaa atc 398
Ser Lys Val Val Arg Ala Lys Glu Arg Leu Asp Glu Glu Leu Lys Ile
100 105 110
cag gcc cag gag gac aga gaa aaa ggg cag atg ccc cat acg tgactgctc 450
Gln Ala Gln Glu Asp Arg Glu Lys Gly Gln Met Pro His Thr
115 120 125
gctccccccg cccaccccgc cgcctctaat ttatagcttg gtaataaatt tcttttctgc 510

<210> 22
<211> 697
<212> DNA
<213> Homo sapiens
<220>
<221> CDS

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<222> (104)...(499)

<400> 22
acttccgggt gttgtctggc cgccgtagcg cgtcttgggt ctcccggctg ccgctgctgc    60
cgccgccgcc tcgggtcgtg gagccaggag cgacgtcacc gcc atg gca ggc atc      115
                                            Met Ala Gly Ile
                                              1

aaa gct ttg att agt ttg tcc ttt gga gga gca atc gga ctg atg ttt      163
Lys Ala Leu Ile Ser Leu Ser Phe Gly Gly Ala Ile Gly Leu Met Phe
  5                  10                  15                  20
ttg atg ctt gga tgt gcc ctt cca ata tac aac aaa tac tgg ccc ctc      211
Leu Met Leu Gly Cys Ala Leu Pro Ile Tyr Asn Lys Tyr Trp Pro Leu
                 25                  30                  35
ttt gtt cta ttt ttt tac atc ctt tca cct att cca tac tgc ata gca      259
Phe Val Leu Phe Phe Tyr Ile Leu Ser Pro Ile Pro Tyr Cys Ile Ala
             40                  45                  50
aga aga tta gtg gat gat aca gat gct atg agt aac gct tgt aag gaa      307
Arg Arg Leu Val Asp Asp Thr Asp Ala Met Ser Asn Ala Cys Lys Glu
         55                  60                  65
ctt gcc atc ttt ctt aca acg ggc att gtc gtg tca gct ttt gga ctc      355
Leu Ala Ile Phe Leu Thr Thr Gly Ile Val Val Ser Ala Phe Gly Leu
     70                  75                  80
cct att gta ttt gcc aga gca cat ctg att gag tgg gga gct tgt gca      403
Pro Ile Val Phe Ala Arg Ala His Leu Ile Glu Trp Gly Ala Cys Ala
 85                  90                  95                 100
ctt gtt ctc aca gga aac aca gtc atc ttt gca act ata cta ggc ttt      451
Leu Val Leu Thr Gly Asn Thr Val Ile Phe Ala Thr Ile Leu Gly Phe
                105                 110                 115
ttc ttg gtc ttt gga agc aat gac gac ttc agc tgg cag cag tgg tgaa     500
Phe Leu Val Phe Gly Ser Asn Asp Asp Phe Ser Trp Gln Gln Trp
            120                 125                 130
aagaaattac tgaactattg tcaaatggac ttcctgtcat ttgttggcca ttcacgcaca    560
caggagatgg ggcagttaat gctgaatggt atagcaagcc tcttgggggt attttaggtg    620
ctcccttctc acttttattg taagcatact attttcacag agacttgctg aaggattaaa    680
aggattttct cttttgg                                                   697
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<210> 23
<211> 1619
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (287)...(1015)

<400> 23
gcagaggccg tcacgtgggt cgccgaggct cgcaagtgcg cgtggccgtg gcggctggtg    60
tggggttgag tcagttgtgg gacccggagc tgctgaccca gcgggtggcc caccgaaccg   120
gtgacacagc ggcaggcgtt agggctcggg agccgcgagc ctggcctcgt cctagagctc   180
ggccgagccg tcgccgccgt cgtcccccgc ccccagtcag caaaccgccg ccgcgggcgc   240
gcccccgctc tgcgctgtct ctccgatggc gtccgcctca ggggcc atg gcg aag      295
                                                   Met Ala Lys
                                                     1
cac gag cag atc ctg gtc ctc gat ccg ccc aca gac ctc aaa ttc aaa     343
His Glu Gln Ile Leu Val Leu Asp Pro Pro Thr Asp Leu Lys Phe Lys
      5                  10                  15
ggc ccc ttc aca gat gta gtc act aca aat ctt aaa ttg cga aat cca     391
Gly Pro Phe Thr Asp Val Val Thr Thr Asn Leu Lys Leu Arg Asn Pro
 20                  25                  30                  35
tcg gat aga aaa gtg tgt ttc aaa gtg aag act aca gca cct cgc cgg     439
Ser Asp Arg Lys Val Cys Phe Lys Val Lys Thr Thr Ala Pro Arg Arg
                 40                  45                  50
tac tgt gtg agg ccc aac agt gga att att gac cca ggg tca act gtg     487
Tyr Cys Val Arg Pro Asn Ser Gly Ile Ile Asp Pro Gly Ser Thr Val
             55                  60                  65
act gtt tca gta atg cta cag ccc ttt gac tat gat ccg aat gaa aag     535
Thr Val Ser Val Met Leu Gln Pro Phe Asp Tyr Asp Pro Asn Glu Lys
         70                  75                  80
agt aaa cac aag ttt atg gta cag aca att ttt gct cca cca aac act     583
Ser Lys His Lys Phe Met Val Gln Thr Ile Phe Ala Pro Pro Asn Thr
     85                  90                  95
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tca gat atg gaa gct gtg tgg aaa gag gca aaa cct gat gaa tta atg      631
Ser Asp Met Glu Ala Val Trp Lys Glu Ala Lys Pro Asp Glu Leu Met
100                 105                 110                 115
gat tcc aaa ttg aga tgc gta ttt gaa atg ccc aat gaa aat gat aaa      679
Asp Ser Lys Leu Arg Cys Val Phe Glu Met Pro Asn Glu Asn Asp Lys
                120                 125                 130
ttg aat gat atg gaa cct agc aaa gct gtt cca ctg aat gca tct aag      727
Leu Asn Asp Met Glu Pro Ser Lys Ala Val Pro Leu Asn Ala Ser Lys
            135                 140                 145
caa gat gga cct atg cca aaa cca cac agt gtt tca ctt aat gat acc      775
Gln Asp Gly Pro Met Pro Lys Pro His Ser Val Ser Leu Asn Asp Thr
        150                 155                 160
gaa aca agg aaa cta atg gaa gag tgt aaa aga ctt cag gga gaa atg      823
Glu Thr Arg Lys Leu Met Glu Glu Cys Lys Arg Leu Gln Gly Glu Met
    165                 170                 175
atg aag cta tca gaa gaa aat cgg cac ctg aga gat gaa ggt tta agg      871
Met Lys Leu Ser Glu Glu Asn Arg His Leu Arg Asp Glu Gly Leu Arg
180                 185                 190                 195
ctc aga aag gta gca cat tcg gat aaa cct gga tca acc tca act gca      919
Leu Arg Lys Val Ala His Ser Asp Lys Pro Gly Ser Thr Ser Thr Ala
                200                 205                 210
tcc ttc aga gat aat gtc acc agt cct ctt cct tca ctt ctt gtt gta      967
Ser Phe Arg Asp Asn Val Thr Ser Pro Leu Pro Ser Leu Leu Val Val
            215                 220                 225
att gca gcc att ttc att gga ttc ttt cta ggg aaa ttc atc ttg         1012
Ile Ala Ala Ile Phe Ile Gly Phe Phe Leu Gly Lys Phe Ile Leu
        230                 235                 240
tagagtgaag catgcagagt gctgtttctt tttttttttt ttctcttgac cagaaaaa     1070
gatttgttta cctaccattt cattggtagt atggcccacg gtgaccattt ttttgtgtgt   1130
acagcgtcat ataggctttg cctttaatga tctcttacgg ttagaaaaca caataaaaac   1190
aaactgttcg gctactggac aggttgtata ttaccagatc atcactagca gatgtcagtt   1250
gcacattgag tcctttatga aattcataaa taaagaattg ttctttcttt gtggttttaa   1310
taagagttca agaattgttc agagtcttgt aaatgttatt ttaataatcc ctttaaattt   1370
tatctgttgc tgttacctct tgaaatatga tttatttaga ttgctaatcc cactcattca   1430
ggaaatgcca agaggtattc cttggggaaa tggtgcctct tacagtgtaa atttttcctc   1490
```



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ctttaccttt gctaatatca tggcagaatt tttcttatcc cttgtgaggc agttgttgac   1550
tgagtttttc atccttacaa tcctgtccca tggtatttaa cataaaaaaa aataaaactg   1610
ttaacagat                                                           1619

<210> 24
<211> 1066
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (65)...(859)

<400> 24
cttcttgctg ccctcgttct tgccggggcc gcggttagtc cctgctggcc accccactgc    60
gacc atg ttc gtt ccc tgc ggg gag tcg gcc ccc gac ctt gcc ggc ttc    109
     Met Phe Val Pro Cys Gly Glu Ser Ala Pro Asp Leu Ala Gly Phe
       1               5                  10                  15
acc ctc cta atg cca gca gta tct gtt gga aat gtt ggc cag ctt gca     157
Thr Leu Leu Met Pro Ala Val Ser Val Gly Asn Val Gly Gln Leu Ala
                 20                  25                  30
atg gat ctg att att tct aca ctg aat atg tct aag att ggt tac ttc     205
Met Asp Leu Ile Ile Ser Thr Leu Asn Met Ser Lys Ile Gly Tyr Phe
             35                  40                  45
tat acc gat tgt ctt gtg cca atg gtt gga aac aat cca tat gcg acc     253
Tyr Thr Asp Cys Leu Val Pro Met Val Gly Asn Asn Pro Tyr Ala Thr
         50                  55                  60
aca gaa gga aat tca aca gaa ctt agc ata aat gct gaa gtg tat tca     301
Thr Glu Gly Asn Ser Thr Glu Leu Ser Ile Asn Ala Glu Val Tyr Ser
     65                  70                  75
ttg cct tca aga aag ctg gtg gct cta cag tta aga tcc att ttt att     349
Leu Pro Ser Arg Lys Leu Val Ala Leu Gln Leu Arg Ser Ile Phe Ile
 80                  85                  90                  95
aag tat aaa tca aag cca ttc tgt gaa aaa ctg ctt tcc tgg gtg aaa     397
Lys Tyr Lys Ser Lys Pro Phe Cys Glu Lys Leu Leu Ser Trp Val Lys
                100                 105                 110
```

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agc agt ggc tgt gcc aga gtc att gtt ctt tcg agc agt cat tca tat      445
Ser Ser Gly Cys Ala Arg Val Ile Val Leu Ser Ser Ser His Ser Tyr
            115                 120                 125
cag cgt aat gat ctg cag ctt cgt agt act ccc ttc cgg tac cta ctt      493
Gln Arg Asn Asp Leu Gln Leu Arg Ser Thr Pro Phe Arg Tyr Leu Leu
        130                 135                 140
aca cct tcc atg caa aaa agt gtt caa aat aaa ata aag agc ctt aac      541
Thr Pro Ser Met Gln Lys Ser Val Gln Asn Lys Ile Lys Ser Leu Asn
    145                 150                 155
tgg gaa gaa atg gaa aaa agc cgg tgc att cct gaa ata gat gat tcc      589
Trp Glu Glu Met Glu Lys Ser Arg Cys Ile Pro Glu Ile Asp Asp Ser
160                 165                 170                 175
gag ttt tgt atc cgc att ccg gga gga ggt atc aca aaa aca ctc tat      637
Glu Phe Cys Ile Arg Ile Pro Gly Gly Gly Ile Thr Lys Thr Leu Tyr
                180                 185                 190
gat gaa agc tgt tct aaa gaa atc caa atg gca gtt ctg ctg aaa ttt      685
Asp Glu Ser Cys Ser Lys Glu Ile Gln Met Ala Val Leu Leu Lys Phe
            195                 200                 205
gtt tca gaa ggg gac aac atc cca gat gca tta ggt ctt gtt gag tat      733
Val Ser Glu Gly Asp Asn Ile Pro Asp Ala Leu Gly Leu Val Glu Tyr
        210                 215                 220
ctt aat gag tgg ctt cag ata ctc aaa cca ctt agc gat gac ccc aca      781
Leu Asn Glu Trp Leu Gln Ile Leu Lys Pro Leu Ser Asp Asp Pro Thr
    225                 230                 235
gta tct gcc tca cgg tgg aaa ata cca agt tct tgg aga tta ctc ttt      829
Val Ser Ala Ser Arg Trp Lys Ile Pro Ser Ser Trp Arg Leu Leu Phe
240                 245                 250                 255
ggc agt ggt ctt ccc cct gca ctt ttc tgatctaatt tctgttttat acct      880
Gly Ser Gly Leu Pro Pro Ala Leu Phe
                260
tatacccaaa acacttacta ccaacacagc tgttaaacat tctatacaaa aaaattgtat      940
gatctggtat taggaaatta ctttcacagt aaatatcaaa gaaaaaagat taagggtctc     1000
tttgccatgc ttttcatcat atgcaccaaa tgtaaatttt gtacaataaa attttatttc     1060
ctaagt                                                                1066
```



```
<210> 25
<211> 618
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (54)...(392)

<400> 25
gtttacgcca gtttgaacca aagacgccca aggttgaggc cgagttccag agc atg        56
                                                           Met
                                                             1
ggg tct cgg ttg tcc cag cct ttt gag tcc tat atc act gcg cct ccc      104
Gly Ser Arg Leu Ser Gln Pro Phe Glu Ser Tyr Ile Thr Ala Pro Pro
            5                  10                  15
ggt acc gcc gcc gcg ccc gcc aaa cct gcg ccc cca gct aca ccc gga      152
Gly Thr Ala Ala Ala Pro Ala Lys Pro Ala Pro Pro Ala Thr Pro Gly
        20                  25                  30
gcg ccg acc tcc cca gca gaa cac cgc ctg ttg aag acc tgc tgg agc      200
Ala Pro Thr Ser Pro Ala Glu His Arg Leu Leu Lys Thr Cys Trp Ser
    35                  40                  45
tgt cgc gtg ctt tct ggg ttg ggc ctg atg ggg gcg ggc ggg tac gtg      248
Cys Arg Val Leu Ser Gly Leu Gly Leu Met Gly Ala Gly Gly Tyr Val
50                  55                  60                  65
tac tgg gtg gca cgg aag ccc atg aag atg gga tac ccc ccg agt cca      296
Tyr Trp Val Ala Arg Lys Pro Met Lys Met Gly Tyr Pro Pro Ser Pro
                70                  75                  80
tgg acc att acg cag atg gtc atc ggc ctc agc att gcc acc tgg ggt      344
Trp Thr Ile Thr Gln Met Val Ile Gly Leu Ser Ile Ala Thr Trp Gly
            85                  90                  95
atc gtt gtc atg gca gac ccc aaa ggg aag gcc tac cgc gtt gtt t        390
Ile Val Val Met Ala Asp Pro Lys Gly Lys Ala Tyr Arg Val Val
        100                 105                 110
gaaagtacca ccagtgaatc tgtcttctgt ctctgtccct ttccccgtga cacacacagc     450
aggcatggaa tttaatgggt gttctggaca gacacttgta catggacaga catcactact     510
```

```
gtggatacta caagactgag aagaaaatcg tatgttgtca ttctctggct atggagtgtt    570
tgtggccttc acagatttca caggaaccaa taaatccctc agagaagt                 618

<210> 26
<211> 1021
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (413)...(853)

<400> 26
aagactataa gccccagcgg gcgacgaccg aacgcccccg ggaacaccgg gccccgagct     60
cggtcccgcg cccgaggatc ctccacgggg ctagatggct gcgtcggggg cgggagcgga    120
ggtgagcggg cgctagggcc gcgagccccc gccggccctt cctccagcgc cctgcggacc    180
ccgcagaagg cgctcgcctc cctagcccgc aaaaacatat cgatttttct cgctgtggca    240
acggggacgt cctgatagat cctctgctcc aataggcaac tccggccttc cctgccctga    300
cctggaacct ctgggagggc tgcagagtaa gtgccgcctc tgcgctccga cggaggcacg    360
aggcctgtgg agtaggtccc tctgttccga caggtgcgac acttggcgct cc atg ctt    418
                                                          Met Leu
                                                            1
gcg ggt gcc ggg agg cct ggc ctc ccc cag ggc cgc cac ctc tgc tgg      466
Ala Gly Ala Gly Arg Pro Gly Leu Pro Gln Gly Arg His Leu Cys Trp
          5                  10                  15
ttg ctc tgt gct ttc acc tta aag ctc tgc caa gca gag gct ccc gtg      514
Leu Leu Cys Ala Phe Thr Leu Lys Leu Cys Gln Ala Glu Ala Pro Val
     20                  25                  30
cag gaa gag aag ctg tca gca agc acc tca aat ttg cca tgc tgg ctg      562
Gln Glu Glu Lys Leu Ser Ala Ser Thr Ser Asn Leu Pro Cys Trp Leu
 35                  40                  45                  50
gtg gaa gag ttt gtg gta gca gaa gag tgc tct cca tgc tct aat ttc      610
Val Glu Glu Phe Val Val Ala Glu Glu Cys Ser Pro Cys Ser Asn Phe
                 55                  60                  65
cgg gct aaa act acc cct gag tgt ggt ccc aca gga tat gta gag aaa      658
Arg Ala Lys Thr Thr Pro Glu Cys Gly Pro Thr Gly Tyr Val Glu Lys
```



```
             70                  75                  80
atc aca tgc agc tca tct aag aga aat gag ttc aaa agc tgc cgc tca      706
Ile Thr Cys Ser Ser Ser Lys Arg Asn Glu Phe Lys Ser Cys Arg Ser
         85                  90                  95
gct ttg atg gaa caa cgc tta ttt tgg aag ttc gaa ggg gct gtc gtg      754
Ala Leu Met Glu Gln Arg Leu Phe Trp Lys Phe Glu Gly Ala Val Val
    100                 105                 110
tgt gtg gcc ctg atc ttc gct tgt ctt gtc atc att cgt cag cga caa      802
Cys Val Ala Leu Ile Phe Ala Cys Leu Val Ile Ile Arg Gln Arg Gln
115                 120                 125                 130
ttg gac aga aag gct ctg gaa aag gtc cgg aag caa atc gag tcc ata      850
Leu Asp Arg Lys Ala Leu Glu Lys Val Arg Lys Gln Ile Glu Ser Ile
                135                 140                 145
tagctacatt ccacccttgt atcctgggtc ttagagaccc tatctcagac agtgaaagtg    910
aaatggactg atttgcactc ttggttcttt ggagccttgt ggtggaatcc ccttttcccc    970
atcttcttct ttcagatcat taatgagcag aataaaaaga gtaaaatggt t            1021

<210> 27
<211> 1432
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (331)...(1365)

<400> 27
atcgcgcccg ggaggcgccg gagcccagcg gctggcgggc cgccgtccca cccccacctc     60
gcccgagtcc ggggcggccc cggtgtcccc tccgagcctg ctgcactcca cgtccccccta   120
ccagggctcc agcccccagg gaaatctccg accaggcccg cccaggagcc agatccaggc    180
tcctggaaga accatgtccg gcagctactg gtcatgccag gcacacactg ctgcccaaga    240
ggagctgctg tttgaattat ctgtgaatgt tgggaagagg aatgccagag ctgccggctg    300
aaaattaccc aaccaagaga aatctgcagg atg gac ttt ctg gtc ctc ttc ttg    354
                                 Met Asp Phe Leu Val Leu Phe Leu
                                   1               5
ttc tac ctg gct tcg gtg ctg atg ggt ctt gtt ctt atc tgc gtc tgc      402
```

```
Phe Tyr Leu Ala Ser Val Leu Met Gly Leu Val Leu Ile Cys Val Cys
    10                  15                  20
tcg aaa acc cat agc ttg aaa ggc ctg gcc agg gga gga gca cag ata      450
Ser Lys Thr His Ser Leu Lys Gly Leu Ala Arg Gly Gly Ala Gln Ile
25                  30                  35                  40
ttt tcc tgt ata att cca gaa tgt ctt cag aga gcc gtg cat gga ttg      498
Phe Ser Cys Ile Ile Pro Glu Cys Leu Gln Arg Ala Val His Gly Leu
                45                  50                  55
ctt cat tac ctt ttc cat acg aga aac cac acc ttc att gtc ctg cac      546
Leu His Tyr Leu Phe His Thr Arg Asn His Thr Phe Ile Val Leu His
            60                  65                  70
ctg gtc ttg caa ggg atg gtt tat act gag tac acc tgg gaa gta ttt      594
Leu Val Leu Gln Gly Met Val Tyr Thr Glu Tyr Thr Trp Glu Val Phe
        75                  80                  85
ggc tac tgt cag gag ctg gag ttg tcc ttg cat tac ctt ctt ctg ccc      642
Gly Tyr Cys Gln Glu Leu Glu Leu Ser Leu His Tyr Leu Leu Leu Pro
    90                  95                  100
tat ctg ctg cta ggt gta aac ctg ttt ttt ttc acc ctg act tgt gga      690
Tyr Leu Leu Leu Gly Val Asn Leu Phe Phe Phe Thr Leu Thr Cys Gly
105                 110                 115                 120
acc aat cct ggc att ata aca aaa gca aat gaa tta tta ttt ctt cat      738
Thr Asn Pro Gly Ile Ile Thr Lys Ala Asn Glu Leu Leu Phe Leu His
                125                 130                 135
gtt tat gaa ttt gat gaa gtg atg ttt cca aag aac gtg agg tgc tct      786
Val Tyr Glu Phe Asp Glu Val Met Phe Pro Lys Asn Val Arg Cys Ser
            140                 145                 150
act tgt gat tta agg aaa cca gct cga tcc aag cac tgc agt gtg tgt      834
Thr Cys Asp Leu Arg Lys Pro Ala Arg Ser Lys His Cys Ser Val Cys
        155                 160                 165
aac tgg tgt gtg cac cgt ttc gac cat cac tgt gtt tgg gtg aac aac      882
Asn Trp Cys Val His Arg Phe Asp His His Cys Val Trp Val Asn Asn
    170                 175                 180
tgc atc ggg gcc tgg aac atc agg tac ttc ctc atc tac gtc ttg acc      930
Cys Ile Gly Ala Trp Asn Ile Arg Tyr Phe Leu Ile Tyr Val Leu Thr
185                 190                 195                 200
```



```
ttg acg gcc tcg gct gcc acc gtc gcc att gtg agc acc act ttt ctg      978
Leu Thr Ala Ser Ala Ala Thr Val Ala Ile Val Ser Thr Thr Phe Leu
                205                 210                 215
gtc cac ttg gtg gtg atg tca gat tta tac cag gag act tac atc gat      1026
Val His Leu Val Val Met Ser Asp Leu Tyr Gln Glu Thr Tyr Ile Asp
            220                 225                 230
gac ctt gga cac ctc cat gtt atg gac acg gtc ttt ctt att cag tac      1074
Asp Leu Gly His Leu His Val Met Asp Thr Val Phe Leu Ile Gln Tyr
        235                 240                 245
ctg ttc ctg act ttt cca cgg att gtc ttc atg ctg ggc ttt gtc gtg      1122
Leu Phe Leu Thr Phe Pro Arg Ile Val Phe Met Leu Gly Phe Val Val
    250                 255                 260
GTT CTG AGC TTC CTC CTG GGT GGC TAC CTG TTG TTT GTC CTG TAT CTG      1170
Val Leu Ser Phe Leu Leu Gly Gly Tyr Leu Leu Phe Val Leu Tyr Leu
265                 270                 275                 280
gcg gcc acc aac cag act act aac gag tgg tac aga ggt gac tgg gcc      1218
Ala Ala Thr Asn Gln Thr Thr Asn Glu Trp Tyr Arg Gly Asp Trp Ala
                285                 290                 295
tgg tgc cag cgt tgt ccc ctt gtg gcc tgg cct ccg tca gca gag ccc      1266
Trp Cys Gln Arg Cys Pro Leu Val Ala Trp Pro Pro Ser Ala Glu Pro
            300                 305                 310
caa gtc cac cgg aac att cac tcc cat ggg ctt cgg agc aac ctt caa      1314
Gln Val His Arg Asn Ile His Ser His Gly Leu Arg Ser Asn Leu Gln
        315                 320                 325
gag atc ttt cta cct gcc ttt cca tgt cat gag agg aag aaa caa gaa      1362
Glu Ile Phe Leu Pro Ala Phe Pro Cys His Glu Arg Lys Lys Gln Glu
    330                 335                 340
tgacaagtgt atgactgcct ttgagctgta gttcccgttt atttacacat gtggatcc      1420
tcgttttcca ag                                                        1432

<210> 28
<211> 601
<212> DNA
<213> Homo sapiens
<220>
```

```
<221> CDS
<222> (62)...(355)

<400> 28
atgcgcacat agcgacttgg tgggcgcgtc cagtgatgac tgggggatcc cggcaagtaa      60
c atg act aaa aag aag cgg gag aat ctg ggc gtc gct cta gag atc gat     109
  Met Thr Lys Lys Lys Arg Glu Asn Leu Gly Val Ala Leu Glu Ile Asp
   1               5                  10                  15
ggg cta gag gag aag ctg tcc cag tgt cgg aga gac ctg gag gcc gtg       157
Gly Leu Glu Glu Lys Leu Ser Gln Cys Arg Arg Asp Leu Glu Ala Val
                20                  25                  30
aac tcc aga ctc cac agc cgg gag ctg agc cca gag gcc agg agg tcc       205
Asn Ser Arg Leu His Ser Arg Glu Leu Ser Pro Glu Ala Arg Arg Ser
            35                  40                  45
ctg gag aag gag aaa aac agc cta atg aac aaa gcc tcc aac tac gag       253
Leu Glu Lys Glu Lys Asn Ser Leu Met Asn Lys Ala Ser Asn Tyr Glu
    50                  55                  60
aag gaa ctg aag ttt ctt cgg caa gag aac cgg aag aac atg ctg ctc       301
Lys Glu Leu Lys Phe Leu Arg Gln Glu Asn Arg Lys Asn Met Leu Leu
65                  70                  75                  80
tct gtg gcc atc ttt atc ctc ctg acg ctc gtc tat gcc tac tgg acc       349
Ser Val Ala Ile Phe Ile Leu Leu Thr Leu Val Tyr Ala Tyr Trp Thr
                85                  90                  95
atg tgagcctggc acttccccac aaccagcaca ggcttccact tggcccct              400
Met

tgatcaggat caagcaggca cttcaagcct caataggacc aaggtgctgg ggtgttcccc     460
tcccaaccta gtgttcaagc atggcttcct ggcggcccag gccttgcctc cctggcctgc     520
tggggggttc cgggtctcca gaaggacatg gtgctggtcc ctcccttagc ccaagggaga     580
ggcaataaag acacaagct g                                                601

<210> 29
<211> 585
<212> DNA
<213> Homo sapiens
```



```
<220>
<221> CDS
<222> (78)...(452)

<400> 29
actaacctct gccctgcagc cgcgagggcg cgcgggaaat cccgagtgca tctggaatac      60
gcagagtcag taagacc atg gct acg tcc tcg atg tct aag ggt tgc ttt        110
                   Met Ala Thr Ser Ser Met Ser Lys Gly Cys Phe
                    1               5                  10
gtt ttt aag cca aac tcc aaa aag aga aag atc tct ctg cca ata gag       158
Val Phe Lys Pro Asn Ser Lys Lys Arg Lys Ile Ser Leu Pro Ile Glu
            15                  20                  25
gac tat ttt aac aaa ggg aaa aat gag cct gag gac agt aag ctt cga       206
Asp Tyr Phe Asn Lys Gly Lys Asn Glu Pro Glu Asp Ser Lys Leu Arg
        30                  35                  40
ttc gaa act tat cag ttg ata tgg cag cag atg aaa tct gaa aat gag       254
Phe Glu Thr Tyr Gln Leu Ile Trp Gln Gln Met Lys Ser Glu Asn Glu
    45                  50                  55
cga cta caa gag gaa tta aat aaa aac ttg ttt gac aat ctg att gaa       302
Arg Leu Gln Glu Glu Leu Asn Lys Asn Leu Phe Asp Asn Leu Ile Glu
60                  65                  70                  75
ttt ctg caa aaa tca cat tct gga ttc cag aag aat tca aga gac ttg       350
Phe Leu Gln Lys Ser His Ser Gly Phe Gln Lys Asn Ser Arg Asp Leu
                80                  85                  90
ggc ggt caa ata aaa ctc aga gaa att cca act gct gct ctt gtt ctt       398
Gly Gly Gln Ile Lys Leu Arg Glu Ile Pro Thr Ala Ala Leu Val Leu
            95                 100                 105
ggt ata tat gcg tat gtt tgt tca tgc atg cat ctc tgt gta ttt cgt       446
Gly Ile Tyr Ala Tyr Val Cys Ser Cys Met His Leu Cys Val Phe Arg
        110                 115                 120
ttt taaatttttt tttattgttg agaatagtgg aaggacctgt tttgatgagc c          500
Phe

tattttgtct ctcttatttg tacaattaaa ccaactatag tttatattac atattttcaa     560
aaaccaataa aaattcctta tcttt                                           585
```

```
<210> 30
<211> 1100
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (57)...(1040)

<400> 30
agaccgacct tgaccgccca cctggcagga gcaggacagg acggccggac gcggcc atg      59
                                                              Met
                                                                1

gcc gag ctc ccg ggg ccc ttt ctc tgc ggg gcc ctg cta ggc ttc ctg       107
Ala Glu Leu Pro Gly Pro Phe Leu Cys Gly Ala Leu Leu Gly Phe Leu
                5                  10                  15
tgc ctg agt ggg ctg gcc gtg gag gtg aag gta ccc aca gag ccg ctg       155
Cys Leu Ser Gly Leu Ala Val Glu Val Lys Val Pro Thr Glu Pro Leu
        20                  25                  30
agc acg ccc ctg ggg aag aca gcc gag ctg acc tgc acc tac agc acg       203
Ser Thr Pro Leu Gly Lys Thr Ala Glu Leu Thr Cys Thr Tyr Ser Thr
    35                  40                  45
tcg gtg gga gac agc ttc gcc ctg gag tgg agc ttt gtg cag cct ggg       251
Ser Val Gly Asp Ser Phe Ala Leu Glu Trp Ser Phe Val Gln Pro Gly
50                  55                  60                  65
aaa ccc atc tct gag tcc cat cca atc ctg tac ttc acc aat ggc cat       299
Lys Pro Ile Ser Glu Ser His Pro Ile Leu Tyr Phe Thr Asn Gly His
                70                  75                  80
ctg tat cca act ggt tct aag tca aag cgg gtc agc ctg ctt cag aac       347
Leu Tyr Pro Thr Gly Ser Lys Ser Lys Arg Val Ser Leu Leu Gln Asn
            85                  90                  95
ccc ccc aca gtg ggg gtg gcc aca ctg aaa ctg act gac gtc cac ccc       395
Pro Pro Thr Val Gly Val Ala Thr Leu Lys Leu Thr Asp Val His Pro
        100                 105                 110
tca gat act gga acc tac ctc tgc caa gtc aac aac cca cca gat ttc       443
```



```
Ser Asp Thr Gly Thr Tyr Leu Cys Gln Val Asn Asn Pro Pro Asp Phe
    115                 120                 125
tac acc aat ggg ttg ggg cta atc aac ctt act gtg ctg gtt ccc ccc       491
Tyr Thr Asn Gly Leu Gly Leu Ile Asn Leu Thr Val Leu Val Pro Pro
130                 135                 140                 145
agt aat ccc tta tgc agt cag agt gga caa acc tct gtg gga ggc tct       539
Ser Asn Pro Leu Cys Ser Gln Ser Gly Gln Thr Ser Val Gly Gly Ser
                150                 155                 160
act gca ctg aga tgc agc tct tcc gag ggg gct cct aag cca gtg tac       587
Thr Ala Leu Arg Cys Ser Ser Ser Glu Gly Ala Pro Lys Pro Val Tyr
            165                 170                 175
aac tgg gtg cgt ctt gga act ttt cct aca cct tct cct ggc agc atg       635
Asn Trp Val Arg Leu Gly Thr Phe Pro Thr Pro Ser Pro Gly Ser Met
        180                 185                 190
gtt caa gat gag gtg tct ggc cag ctc att ctc acc aac ctc tcc ctg       683
Val Gln Asp Glu Val Ser Gly Gln Leu Ile Leu Thr Asn Leu Ser Leu
    195                 200                 205
acc tcc tcg ggc acc tac cgc tgt gtg gcc acc aac cag atg ggc agt       731
Thr Ser Ser Gly Thr Tyr Arg Cys Val Ala Thr Asn Gln Met Gly Ser
210                 215                 220                 225
gca tcc tgt gag ctg acc ctc tct gtg acc gaa ccc tcc caa ggc cga       779
Ala Ser Cys Glu Leu Thr Leu Ser Val Thr Glu Pro Ser Gln Gly Arg
                230                 235                 240
gtg gcc gga gct ctg att ggg gtg ctc ctg ggc gtg ctg ttg ctg tca       827
Val Ala Gly Ala Leu Ile Gly Val Leu Leu Gly Val Leu Leu Leu Ser
            245                 250                 255
gtt gct gcg ttc tgc ctg gtc agg ttc cag aaa gag agg ggg aag aag       875
Val Ala Ala Phe Cys Leu Val Arg Phe Gln Lys Glu Arg Gly Lys Lys
        260                 265                 270
ccc aag gag aca tat ggg ggt agt gac ctt cgg gag gat gcc atc gct       923
Pro Lys Glu Thr Tyr Gly Gly Ser Asp Leu Arg Glu Asp Ala Ile Ala
    275                 280                 285
cct ggg atc tct gag cac act tgt atg agg gct gat tct agc aag ggg       971
Pro Gly Ile Ser Glu His Thr Cys Met Arg Ala Asp Ser Ser Lys Gly
290                 295                 300                 305
```

```
ttc ctg gaa aga ccc tcg tct gcc agc acc gtg acg acc acc aag tcc     1019
Phe Leu Glu Arg Pro Ser Ser Ala Ser Thr Val Thr Thr Thr Lys Ser
                310                 315                 320
aag ctc cct atg gtc gtg tgacttctcc cgatccctga gggcggtgag ggg        1070
Lys Leu Pro Met Val Val
            325
gaatatcaat aattaaagtc tgtgggtacc                                    1100

<210> 31
<211> 313
<212> PRT
<213> Homo sapiens

<400> 31
Met Asn Gln Leu Ser Phe Leu Leu Phe Leu Ile Ala Thr Thr Arg Gly
 1               5                  10                  15
Trp Ser Thr Asp Glu Ala Asn Thr Tyr Phe Lys Glu Trp Thr Cys Ser
            20                  25                  30
Ser Ser Pro Ser Leu Pro Arg Ser Cys Lys Glu Ile Lys Asp Glu Cys
        35                  40                  45
Pro Ser Ala Phe Asp Gly Leu Tyr Phe Leu Arg Thr Glu Asn Gly Val
    50                  55                  60
Ile Tyr Gln Thr Phe Cys Asp Met Thr Ser Gly Gly Gly Gly Trp Thr
65                  70                  75                  80
Leu Val Ala Ser Val His Glu Asn Asp Met Arg Gly Lys Cys Thr Val
                85                  90                  95
Gly Asp Arg Trp Ser Ser Gln Gln Gly Ser Lys Ala Asp Tyr Pro Glu
            100                 105                 110
Gly Asp Gly Asn Trp Ala Asn Tyr Asn Thr Phe Gly Ser Ala Glu Ala
        115                 120                 125
Ala Thr Ser Asp Asp Tyr Lys Asn Pro Gly Tyr Tyr Asp Ile Gln Ala
    130                 135                 140
Lys Asp Leu Gly Ile Trp His Val Pro Asn Lys Ser Pro Met Gln His
145                 150                 155                 160
Trp Arg Asn Ser Ser Leu Leu Arg Tyr Arg Thr Asp Thr Gly Phe Leu
```



```
                165                 170                 175
Gln Thr Leu Gly His Asn Leu Phe Gly Ile Tyr Gln Lys Tyr Pro Val
            180                 185                 190
Lys Tyr Gly Glu Gly Lys Cys Trp Thr Asp Asn Gly Pro Val Ile Pro
        195                 200                 205
Val Val Tyr Asp Phe Gly Asp Ala Gln Lys Thr Ala Ser Tyr Tyr Ser
    210                 215                 220
Pro Tyr Gly Gln Arg Glu Phe Thr Ala Gly Phe Val Gln Phe Arg Val
225                 230                 235                 240
Phe Asn Asn Glu Arg Ala Ala Asn Ala Leu Cys Ala Gly Met Arg Val
                245                 250                 255
Thr Gly Cys Asn Thr Glu His His Cys Ile Gly Gly Gly Gly Tyr Phe
            260                 265                 270
Pro Glu Ala Ser Pro Gln Gln Cys Gly Asp Phe Ser Gly Phe Asp Trp
        275                 280                 285
Ser Gly Tyr Gly Thr His Val Gly Tyr Ser Ser Ser Arg Glu Ile Thr
    290                 295                 300
Glu Ala Ala Val Leu Leu Phe Tyr Arg
305                 310

<210> 32
<211> 229
<212> PRT
<213> Homo sapiens

<400> 32
Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala
 1               5                  10                  15
Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
            20                  25                  30
Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
        35                  40                  45
Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
    50                  55                  60
Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu
```

```
65                  70                  75                  80
Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
                85                  90                  95
Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe
            100                 105                 110
Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn
        115                 120                 125
Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr
    130                 135                 140
Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Glu Ser Ile
145                 150                 155                 160
Asn Ser Ile Lys Ser Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu
                165                 170                 175
Leu Arg Ala Phe Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe
            180                 185                 190
Asp Arg Val Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val
        195                 200                 205
Val Ser Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys
    210                 215                 220
Arg Lys Ser Arg Thr
225
```

<210> 33
<211> 467
<212> PRT
<213> Homo sapiens

<400> 33

```
Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu
1               5                   10                  15
Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr
            20                  25                  30
Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala
        35                  40                  45
Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe
```



```
    50                  55                  60
Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys
65                  70                  75                  80
Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro
                85                  90                  95
Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe
            100                 105                 110
Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr
        115                 120                 125
Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser
    130                 135                 140
Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp
145                 150                 155                 160
Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg
                165                 170                 175
Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu
            180                 185                 190
Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys
        195                 200                 205
Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val
    210                 215                 220
Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser
225                 230                 235                 240
Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr
                245                 250                 255
Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly
            260                 265                 270
Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro
        275                 280                 285
His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr
    290                 295                 300
Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val
305                 310                 315                 320
Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn
            325                 330                 335
```

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg
340 345 350
Leu Arg Gln Met Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr
355 360 365
Glu Thr His Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val
370 375 380
Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu
385 390 395 400
Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile
405 410 415
Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn
420 425 430
Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu
435 440 445
Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr
450 455 460
Asn Val Ile
465

<210> 34
<211> 99
<212> PRT
<213> Homo sapiens

<400> 34
Met Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser
1 5 10 15
Val Lys Gly His Val Lys Met Leu Arg Leu Asp Ile Ile Asn Ser Leu
20 25 30
Val Thr Thr Val Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro
35 40 45
Glu Thr Thr Thr Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr
50 55 60
Ala Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu
65 70 75 80

Phe Asn Pro Ser Gly Pro Tyr Gln Gln Lys Pro Val His Glu Lys Lys
85 90 95
Glu Val Leu

<210> 35
<211> 189
<212> PRT
<213> Homo sapiens

<400> 35
Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu
1 5 10 15
Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val
20 25 30
Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu
35 40 45
Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys
50 55 60
Ala Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln
65 70 75 80
Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser Leu
85 90 95
Thr Leu Ala Thr Val Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr Ala
100 105 110
Ala Met Trp Ala Leu Gln Thr Val Glu Lys Glu Arg Gly Leu Gly Gly
115 120 125
Glu Val Pro Gly Ser His Gln Gly Pro Asp Pro Tyr Arg Gln Leu Arg
130 135 140
Glu Lys Asp Pro Lys Tyr Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr
145 150 155 160
His Gly Leu Ser Ser Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly
165 170 175
Leu Cys Leu Ala Gly Leu Ala Leu Glu Ile Arg Ser Leu
180 185

```
<210> 36
<211> 363
<212> PRT
<213> Homo sapiens

<400> 36
Met Val Asp Ser Leu Leu Ala Val Thr Leu Ala Gly Asn Leu Gly Leu
  1               5                  10                  15
Thr Phe Leu Arg Gly Ser Gln Thr Gln Ser His Pro Asp Leu Gly Thr
             20                  25                  30
Glu Gly Cys Trp Asp Gln Leu Ser Ala Pro Arg Thr Phe Thr Leu Leu
         35                  40                  45
Asp Pro Lys Ala Ser Leu Leu Thr Lys Ala Phe Leu Asn Gly Ala Leu
     50                  55                  60
Asp Gly Val Ile Leu Gly Asp Tyr Leu Ser Arg Thr Pro Glu Pro Arg
 65                  70                  75                  80
Pro Ser Leu Ser His Leu Leu Ser Gln Tyr Tyr Gly Ala Gly Val Ala
                 85                  90                  95
Arg Asp Pro Gly Phe Arg Ser Asn Phe Arg Arg Gln Asn Gly Ala Ala
            100                 105                 110
Leu Thr Ser Ala Ser Ile Leu Ala Gln Gln Val Trp Gly Thr Leu Val
        115                 120                 125
Leu Leu Gln Arg Leu Glu Pro Val His Leu Gln Leu Gln Cys Met Ser
    130                 135                 140
Gln Glu Gln Leu Ala Gln Val Ala Ala Asn Ala Thr Lys Glu Phe Thr
145                 150                 155                 160
Glu Ala Phe Leu Gly Cys Pro Ala Ile His Pro Arg Cys Arg Trp Gly
                165                 170                 175
Ala Ala Pro Tyr Arg Gly Arg Pro Lys Leu Leu Gln Leu Pro Leu Gly
            180                 185                 190
Phe Leu Tyr Val His His Thr Tyr Val Pro Ala Pro Pro Cys Thr Asp
        195                 200                 205
Phe Thr Arg Cys Ala Ala Asn Met Arg Ser Met Gln Arg Tyr His Gln
    210                 215                 220
Asp Thr Gln Gly Trp Gly Asp Ile Gly Tyr Ser Phe Val Val Gly Ser
```



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225                 230                 235                 240
Asp Gly Tyr Val Tyr Glu Gly Arg Gly Trp His Trp Val Gly Ala His
                245                 250                 255
Thr Leu Gly His Asn Ser Arg Gly Phe Gly Val Ala Ile Val Gly Asn
            260                 265                 270
Tyr Thr Ala Ala Leu Pro Thr Glu Ala Ala Leu Arg Thr Val Arg Asp
        275                 280                 285
Thr Leu Pro Ser Cys Ala Val Arg Ala Gly Leu Leu Arg Pro Asp Tyr
    290                 295                 300
Ala Leu Leu Gly His Arg Gln Leu Val Arg Thr Asp Cys Pro Gly Asp
305                 310                 315                 320
Ala Leu Phe Asp Leu Leu Arg Thr Trp Pro His Phe Thr Ala Thr Val
                325                 330                 335
Lys Pro Arg Pro Ala Arg Ser Val Ser Lys Arg Ser Arg Arg Glu Pro
            340                 345                 350
Pro Pro Arg Thr Leu Pro Ala Thr Asp Leu Gln
        355                 360

<210> 37
<211> 249
<212> PRT
<213> Homo sapiens

<400> 37
Met Gly Gly Pro Arg Gly Ala Gly Trp Val Ala Ala Gly Leu Leu Leu
  1               5                  10                  15
Gly Ala Gly Ala Cys Tyr Cys Ile Tyr Arg Leu Thr Arg Gly Arg Arg
             20                  25                  30
Arg Gly Asp Arg Glu Leu Gly Ile Arg Ser Ser Lys Ser Ala Glu Asp
         35                  40                  45
Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala Glu Gln Leu Gln
     50                  55                  60
Lys Leu Leu Tyr Leu Leu Glu Ser Thr Glu Asp Pro Val Ile Ile Glu
 65                  70                  75                  80
Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe Ser Val Asn Gln
```

```
                    85                  90                  95
Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val Ala Asn Lys Ile
            100                 105                 110
Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu Asn Ala Leu Asn
        115                 120                 125
Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile Lys Val Gln Val
    130                 135                 140
Leu Lys Leu Leu Leu Asn Leu Ser Glu Asn Pro Ala Met Thr Glu Gly
145                 150                 155                 160
Leu Leu Arg Ala Gln Val Asp Ser Ser Phe Leu Ser Leu Tyr Asp Ser
                165                 170                 175
His Val Ala Lys Glu Ile Leu Leu Arg Val Leu Thr Leu Phe Gln Asn
            180                 185                 190
Ile Lys Asn Cys Leu Lys Ile Glu Gly His Leu Ala Val Gln Pro Thr
        195                 200                 205
Phe Thr Glu Gly Ser Leu Phe Phe Leu Leu His Gly Glu Glu Cys Ala
    210                 215                 220
Gln Lys Ile Arg Ala Leu Val Asp His His Asp Ala Glu Val Lys Glu
225                 230                 235                 240
Lys Val Val Thr Ile Ile Pro Lys Ile
                245
```

<210> 38
<211> 98
<212> PRT
<213> Homo sapiens

<400> 38

```
Met Ala Ser Leu Leu Cys Cys Gly Pro Lys Leu Ala Ala Cys Gly Ile
  1               5                  10                  15
Val Leu Ser Ala Trp Gly Val Ile Met Leu Ile Met Leu Gly Ile Phe
             20                  25                  30
Phe Asn Val His Ser Ala Val Leu Ile Glu Asp Val Pro Phe Thr Glu
         35                  40                  45
Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile Tyr Asn Leu Tyr Glu Gln
```



```
     50                  55                  60
Val Ser Tyr Asn Cys Phe Ile Ala Ala Gly Leu Tyr Leu Leu Leu Gly
 65                  70                  75                  80
Gly Phe Ser Phe Cys Gln Val Arg Leu Asn Lys Arg Lys Glu Tyr Met
                 85                  90                  95
Val Arg
```

<210> 39
<211> 172
<212> PRT
<213> Homo sapiens

<400> 39

```
Met Val Gly Pro Ala Pro Arg Arg Arg Leu Arg Pro Leu Ala Ala Leu
  1               5                  10                  15
Ala Leu Val Leu Ala Leu Ala Pro Gly Leu Pro Thr Ala Arg Ala Gly
             20                  25                  30
Gln Thr Pro Arg Pro Ala Glu Arg Gly Pro Pro Val Arg Leu Phe Thr
         35                  40                  45
Glu Glu Glu Leu Ala Arg Tyr Gly Gly Glu Glu Glu Asp Gln Pro Ile
     50                  55                  60
Tyr Leu Ala Val Lys Gly Val Val Phe Asp Val Thr Ser Gly Lys Glu
 65                  70                  75                  80
Phe Tyr Gly Arg Gly Ala Pro Tyr Asn Ala Leu Thr Gly Lys Asp Ser
                 85                  90                  95
Thr Arg Gly Val Ala Lys Met Ser Leu Asp Pro Ala Asp Leu Thr His
            100                 105                 110
Asp Thr Thr Gly Leu Thr Ala Lys Glu Leu Glu Ala Leu Asp Glu Val
        115                 120                 125
Phe Thr Lys Val Tyr Lys Ala Lys Tyr Pro Ile Val Gly Tyr Thr Ala
    130                 135                 140
Arg Arg Ile Leu Asn Glu Asp Gly Ser Pro Asn Leu Asp Phe Lys Pro
145                 150                 155                 160
Glu Asp Gln Pro His Phe Asp Ile Lys Asp Glu Phe
                165                 170
```

<210> 40
<211> 120
<212> PRT
<213> Homo sapiens

<400> 40
Met Met Pro Ser Arg Thr Asn Leu Ala Thr Gly Ile Pro Ser Ser Lys
1 5 10 15
Val Lys Tyr Ser Arg Leu Ser Ser Thr Asp Asp Gly Tyr Ile Asp Leu
20 25 30
Gln Phe Lys Lys Thr Pro Pro Lys Ile Pro Tyr Lys Ala Ile Ala Leu
35 40 45
Ala Thr Val Leu Phe Leu Ile Gly Ala Phe Leu Ile Ile Ile Gly Ser
50 55 60
Leu Leu Leu Ser Gly Tyr Ile Ser Lys Gly Gly Ala Asp Arg Ala Val
65 70 75 80
Pro Val Leu Ile Ile Gly Ile Leu Val Phe Leu Pro Gly Phe Tyr His
85 90 95
Leu Arg Ile Ala Tyr Tyr Ala Ser Lys Gly Tyr Arg Gly Tyr Ser Tyr
100 105 110
Asp Asp Ile Pro Asp Phe Asp Asp
115 120

<210> 41
<211> 939
<212> DNA
<213> Homo sapiens

<400> 41
atgaaccaac tcagcttcct gctgtttctc atagcgacca ccagaggatg gagtacagat 60
gaggctaata cttacttcaa ggaatggacc tgttcttcgt ctccatctct gcccagaagc 120
tgcaaggaaa tcaaagacga atgtcctagt gcatttgatg gcctgtattt tctccgcact 180
gagaatggtg ttatctacca gaccttctgt gacatgacct ctgggggtgg cggctggacc 240
ctggtggcca gcgtgcatga gaatgacatg cgtgggaagt gcacggtggg cgatcgctgg 300

tccagtcagc agggcagcaa agcagactac ccagaggggg acggcaactg ggccaactac 360
aacacctttg gatctgcaga ggcggccacg agcgatgact acaagaaccc tggctactac 420
gacatccagg ccaaggacct gggcatctgg cacgtgccca ataagtcccc catgcagcac 480
tggagaaaca gctccctgct gaggtaccgc acggacactg gcttcctcca gacactggga 540
cataatctgt ttggcatcta ccagaaatat ccagtgaaat atggagaagg aaagtgttgg 600
actgacaacg gcccggtgat ccctgtggtc tatgattttg gcgacgccca gaaaacagca 660
tcttattact caccctatgg ccagcgggaa ttcactgcgg gatttgttca gttcagggta 720
tttaataacg agagagcagc caacgccttg tgtgctggaa tgagggtcac cggatgtaac 780
actgagcacc actgcattgg tggaggagga tactttccag aggccagtcc ccagcagtgt 840
ggagattttt ctggttttga ttggagtgga tatggaactc atgttggtta cagcagcagc 900
cgtgagataa ctgaggcagc tgtgcttcta ttctatcgt 939

<210> 42
<211> 687
<212> DNA
<213> Homo sapiens

<400> 42
atgggcgaca agatctggct gcccttcccc gtgctccttc tggccgctct gcctccggtg 60
ctgctgcctg gggcggccgg cttcacacct tccctcgata gcgacttcac ctttaccctt 120
cccgccggcc agaaggagtg cttctaccag cccatgcccc tgaaggcctc gctggagatc 180
gagtaccaag ttttagatgg agcaggatta gatattgatt tccatcttgc ctctccagaa 240
ggcaaaacct tagtttttga acaaagaaaa tcagatggag ttcacactgt agagactgaa 300
gttggtgatt acatgttctg ctttgacaat acattcagca ccatttctga gaaggtgatt 360
ttctttgaat taatcctgga taatatggga gaacaggcac aagaacaaga agattggaag 420
aaatatatta ctggcacaga tatattggat atgaaactgg aagacatcct ggaatccatc 480
aacagcatca agtccagact aagcaaaagt gggcacatac aaattctgct tagagcattt 540
gaagctcgtg atcgaaacat acaagaaagc aactttgata gagtcaattt ctggtctatg 600
gttaatttag tggtcatggt ggtggtgtca gccattcaag tttatatgct gaagagtctg 660
tttgaagata agaggaaaag tagaact 687

<210> 43
<211> 1401
<212> DNA
<213> Homo sapiens

<400> 43
atgcggcccc aggagctccc caggctcgcg ttcccgttgc tgctgttgct gttgctgctg 60
ctgccgccgc cgccgtgccc tgcccacagc gccacgcgct tcgaccccac ctgggagtcc 120
ctggacgccc gccagctgcc cgcgtggttt gaccaggcca agttcggcat cttcatccac 180
tggggagtgt tttccgtgcc cagcttcggt agcgagtggt tctggtggta ttggcaaaag 240
gaaaagatac cgaagtatgt ggaatttatg aaagataatt accctcctag tttcaaatat 300
gaagattttg gaccactatt tacagcaaaa ttttttaatg ccaaccagtg ggcagatatt 360
tttcaggcct ctggtgccaa atacattgtc ttaacttcca aacatcatga aggctttacc 420
ttgtgggggt cagaatattc gtggaactgg aatgccatag atgaggggcc caagagggac 480
attgtcaagg aacttgaggt agccattagg aacagaactg acctgcgttt tggactgtac 540
tattcccttt ttgaatggtt tcatccgctc ttccttgagg atgaatccag ttcattccat 600
aagcggcaat ttccagtttc taagacattg ccagagctct atgagttagt gaacaactat 660
cagcctgagg ttctgtggtc ggatggtgac ggaggagcac cggatcaata ctggaacagc 720
acaggcttct tggcctggtt atataatgaa agcccagttc ggggcacagt agtcaccaat 780
gatcgttggg gagctggtag catctgtaag catggtggct tctatacctg cagtgatcgt 840
tataacccag gacatctttt gccacataaa tgggaaaact gcatgacaat agacaaactg 900
tcctggggct ataggaggga agctggaatc tctgactatc ttacaattga agaattggtg 960
aagcaacttg tagagacagt ttcatgtgga ggaaatcttt tgatgaatat tgggcccaca 1020
ctagatggca ccatttctgt agtttttgag gagcgactga ggcaaatggg gtcctggcta 1080
aaagtcaatg gagaagctat ttatgaaacc catacctggc gatcccagaa tgacactgtc 1140
accccagatg tgtggtacac atccaagcct aaagaaaaat tagtctatgc cattttttctt 1200
aaatggccca catcaggaca gctgttcctt ggccatccca aagctattct gggggcaaca 1260
gaggtgaaac tactgggcca tggacagcca cttaactgga tttctttgga gcaaaatggc 1320
attatggtag aactgccaca gctaaccatt catcagatgc cgtgtaaatg ggctgggct 1380
ctagccctga ctaatgtgat c 1401

<210> 44
<211> 297
<212> DNA
<213> Homo sapiens

<400> 44
atggataacg tgcagccgaa aataaaacat cgcccctcct gcttcagtgt gaaaggccac 60
gtgaagatgc tgcggctgga tattatcaac tcactggtaa caacagtatt catgctcatc 120

gtatctgtgt tggcactgat accagaaacc acaacattga cagttggtgg aggggtgttt 180
gcacttgtga cagcagtatg ctgtcttgcc gacggggccc ttatttaccg gaagcttctg 240
ttcaatccca gcggtcctta ccagcaaaag cctgtgcatg aaaaaaaaga agttttg 297

<210> 45
<211> 567
<212> DNA
<213> Homo sapiens

<400> 45
atggaggaag gcgggaacct aggaggcctg attaagatgg tccatctact ggtcttgtca 60
ggtgcctggg gcatgcaaat gtgggtgacc ttcgtctcag gcttcctgct tttccgaagc 120
cttccccgac ataccttcgg actagtgcag agcaaactct tccccttcta cttccacatc 180
tccatgggct gtgccttcat caacctctgc atcttggctt cacagcatgc ttgggctcag 240
ctcacattct gggaggccag ccagctttac ctgctgttcc tgagccttac gctggccact 300
gtcaacgccc gctggctgga accccgcacc acagctgcca tgtgggccct gcaaaccgtg 360
gagaaggagc gaggcctggg tggggaggta ccaggcagcc accagggtcc cgatccctac 420
cgccagctgc gagagaagga ccccaagtac agtgctctcc gccagaattt cttccgctac 480
catgggctgt cctctctttg caatctgggc tgcgtcctga gcaatgggct ctgtctcgct 540
ggccttgccc tggaaataag gagcctc 567

<210> 46
<211> 1089
<212> DNA
<213> Homo sapiens

<400> 46
atggtggaca gcctcctggc agtcaccctg gctggaaacc tgggcctgac cttcctccga 60
ggttcccaga cccagagcca tccagacctg ggaactgagg gctgctggga ccagctctct 120
gcccctcgga cctttacgct tttggacccc aaggcatctc tgttaaccaa ggccttcctc 180
aatggcgccc tggatggggt catccttgga gactacctga gccggactcc tgagccccgg 240
ccatccctca gccacttgct gagccagtac tatggggctg gggtggccag agacccaggg 300
ttccgcagca acttccgacg gcagaacggt gctgctctga cttcagcctc catcctggcc 360
cagcaggtgt ggggaaccct tgtccttcta cagaggctgg agccagtaca cctccagctt 420
cagtgcatga gccaagaaca gctggcccag gtggctgcca atgctaccaa ggaattcact 480

gaggccttcc tgggatgccc ggccatccac ccccgctgcc gctggggagc ggcgccttat 540
cggggccgcc cgaagctgct gcagctgccg ctgggattct tgtacgtgca tcacacctac 600
gtgcctgcac caccctgcac ggacttcacg cgctgcgcag ccaacatgcg ctccatgcag 660
cgctaccacc aggacacgca aggctgggga gacatcggct acagtttcgt ggtgggctcg 720
gacggctacg tgtacgaggg acgcggctgg cactgggtgg gcgcccacac gctcggccac 780
aactcccggg gcttcggcgt ggccatagtg ggcaactaca ccgcggcgct gcccaccgag 840
gccgctctgc gcacggtgcg cgacacgctc ccgagttgtg cggtgcgcgc cggcctcctg 900
cggccagact acgcgctgct gggccaccgc cagctggtgc gcaccgactg ccccggcgac 960
gcgctcttcg acctgctgcg cacctggccg cacttcaccg cgactgttaa gccaagacct 1020
gccaggagtg tctctaagag atccaggagg gagccacccc caaggaccct gccagccaca 1080
gacctccaa 1089

<210> 47
<211> 747
<212> DNA
<213> Homo sapiens

<400> 47
atgggtggcc cccggggcgc gggctgggtg gcggcgggcc tgctgctcgg cgcgggcgcc 60
tgctactgca tttacaggct gacccggggt cggcggcggg gcgaccgcga gctcgggata 120
cgctcttcga agtccgcaga agacttaact gatggttcat atgatgatgt tctaaatgct 180
gaacaacttc agaaactcct ttacctgctg gagtcaacgg aggatcctgt aattattgaa 240
agagctttga ttactttggg taacaatgca gccttttcag ttaaccaagc tattattcgt 300
gaattgggtg gtattccaat tgttgcaaac aaaatcaacc attccaacca gagtattaaa 360
gagaaagctt taaatgcact aaataacctg agtgtgaatg ttgaaaatca aatcaagata 420
aaggtgcaag ttttgaaact gcttttgaat ttgtctgaaa atccagccat gacagaagga 480
cttctccgtg cccaagtgga ttcatcattc ctttcccttt atgacagcca cgtagcaaag 540
gagattcttc ttcgagtact tacgctattt cagaatataa agaactgcct caaaatagaa 600
ggccatttag ctgtgcagcc tactttcact gaaggttcat tgtttttcct gttacatgga 660
gaagaatgtg cccagaaaat aagagcttta gttgatcacc atgatgcaga ggtgaaggaa 720
aaggttgtaa caataatacc caaaatc 747

<210> 48
<211> 294
<212> DNA

<213> Homo sapiens

<400> 48
atggcgtcgc tcctgtgctg tgggccgaag ctggccgcct gcggcatcgt cctcagcgcc 60
tggggagtga tcatgttgat aatgctcgga atatttttca atgtccattc cgctgtgttg 120
attgaggacg ttcccttcac ggagaaagat tttgagaatg gcccccagaa catatacaac 180
ctttacgagc aagtcagcta caactgtttc atcgctgcag gcctttacct cctcctcgga 240
ggcttctctt tctgccaagt tcggctcaat aagcgcaagg aatacatggt gcgc 294

<210> 49
<211> 516
<212> DNA
<213> Homo sapiens

<400> 49
atggtgggcc ccgcgccgcg gcggcggctg cggccgctgg cagcgctggc cctggtcctg 60
gcgctggccc cggggctgcc cacagcccgg gccgggcaga caccgcgccc tgccgagcgg 120
gggcccccag tgcggctttt caccgaggag gagctggccc gctatggcgg ggaggaggaa 180
gatcagccca tctacttggc agtgaaggga gtggtgtttg atgtcacctc cggaaaggag 240
ttttatggac gaggagcccc ctacaatgcc ttgacgggga aggactccac tagaggggta 300
gccaagatgt ccttggatcc tgcagacctc acccatgaca ctacgggtct cacggccaag 360
gaactggagg ccctggatga ggtcttcacc aaagtgtaca aagccaaata ccccatcgtc 420
ggctacactg cccggagaat tctcaatgag gatggcagcc ctaacctgga cttcaagcct 480
gaagaccagc cccattttga catcaaggat gagttc 516

<210> 50
<211> 360
<212> DNA
<213> Homo sapiens

<400> 50
atgatgccgt cccgtaccaa cctggctact ggaatcccca gtagtaaagt gaaatattca 60
aggctctcca gcacagacga tggctacatt gaccttcagt ttaagaaaac ccctcctaag 120
atcccttata aggccatcgc acttgccact gtgctgtttt tgattggcgc ctttctcatt 180
attataggct ccctcctgct gtcaggctac atcagcaaag ggggggcaga ccgggccgtt 240

```
ccagtgctga tcattggcat tctggtgttc ctacccggat tttaccacct gcgcatcgct     300
tactatgcat ccaaaggcta ccgtggttac tcctatgatg acattccaga ctttgatgac     360
```

<210> 51
<211> 1065
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (2)...(943)

<400> 51

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a atg aac caa ctc agc ttc ctg ctg ttt ctc ata gcg acc acc aga gga      49
  Met Asn Gln Leu Ser Phe Leu Leu Phe Leu Ile Ala Thr Thr Arg Gly
    1               5                  10                  15
tgg agt aca gat gag gct aat act tac ttc aag gaa tgg acc tgt tct        97
Trp Ser Thr Asp Glu Ala Asn Thr Tyr Phe Lys Glu Trp Thr Cys Ser
            20                  25                  30
tcg tct cca tct ctg ccc aga agc tgc aag gaa atc aaa gac gaa tgt       145
Ser Ser Pro Ser Leu Pro Arg Ser Cys Lys Glu Ile Lys Asp Glu Cys
        35                  40                  45
cct agt gca ttt gat ggc ctg tat ttt ctc cgc act gag aat ggt gtt       193
Pro Ser Ala Phe Asp Gly Leu Tyr Phe Leu Arg Thr Glu Asn Gly Val
    50                  55                  60
atc tac cag acc ttc tgt gac atg acc tct ggg ggt ggc ggc tgg acc       241
Ile Tyr Gln Thr Phe Cys Asp Met Thr Ser Gly Gly Gly Gly Trp Thr
65                  70                  75                  80
ctg gtg gcc agc gtg cat gag aat gac atg cgt ggg aag tgc acg gtg       289
Leu Val Ala Ser Val His Glu Asn Asp Met Arg Gly Lys Cys Thr Val
                85                  90                  95
ggc gat cgc tgg tcc agt cag cag ggc agc aaa gca gac tac cca gag       337
Gly Asp Arg Trp Ser Ser Gln Gln Gly Ser Lys Ala Asp Tyr Pro Glu
            100                 105                 110
ggg gac ggc aac tgg gcc aac tac aac acc ttt gga tct gca gag gcg       385
Gly Asp Gly Asn Trp Ala Asn Tyr Asn Thr Phe Gly Ser Ala Glu Ala
```



```
        115                 120                 125
gcc acg agc gat gac tac aag aac cct ggc tac tac gac atc cag gcc       433
Ala Thr Ser Asp Asp Tyr Lys Asn Pro Gly Tyr Tyr Asp Ile Gln Ala
    130                 135                 140
aag gac ctg ggc atc tgg cac gtg ccc aat aag tcc ccc atg cag cac       481
Lys Asp Leu Gly Ile Trp His Val Pro Asn Lys Ser Pro Met Gln His
145                 150                 155                 160
tgg aga aac agc tcc ctg ctg agg tac cgc acg gac act ggc ttc ctc       529
Trp Arg Asn Ser Ser Leu Leu Arg Tyr Arg Thr Asp Thr Gly Phe Leu
                165                 170                 175
cag aca ctg gga cat aat ctg ttt ggc atc tac cag aaa tat cca gtg       577
Gln Thr Leu Gly His Asn Leu Phe Gly Ile Tyr Gln Lys Tyr Pro Val
            180                 185                 190
aaa tat gga gaa gga aag tgt tgg act gac aac ggc ccg gtg atc cct       625
Lys Tyr Gly Glu Gly Lys Cys Trp Thr Asp Asn Gly Pro Val Ile Pro
        195                 200                 205
gtg gtc tat gat ttt ggc gac gcc cag aaa aca gca tct tat tac tca       673
Val Val Tyr Asp Phe Gly Asp Ala Gln Lys Thr Ala Ser Tyr Tyr Ser
    210                 215                 220
ccc tat ggc cag cgg gaa ttc act gcg gga ttt gtt cag ttc agg gta       721
Pro Tyr Gly Gln Arg Glu Phe Thr Ala Gly Phe Val Gln Phe Arg Val
225                 230                 235                 240
ttt aat aac gag aga gca gcc aac gcc ttg tgt gct gga atg agg gtc       769
Phe Asn Asn Glu Arg Ala Ala Asn Ala Leu Cys Ala Gly Met Arg Val
                245                 250                 255
acc gga tgt aac act gag cac cac tgc att ggt gga gga gga tac ttt       817
Thr Gly Cys Asn Thr Glu His His Cys Ile Gly Gly Gly Gly Tyr Phe
            260                 265                 270
cca gag gcc agt ccc cag cag tgt gga gat ttt tct ggt ttt gat tgg       865
Pro Glu Ala Ser Pro Gln Gln Cys Gly Asp Phe Ser Gly Phe Asp Trp
        275                 280                 285
agt gga tat gga act cat gtt ggt tac agc agc agc cgt gag ata act       913
Ser Gly Tyr Gly Thr His Val Gly Tyr Ser Ser Ser Arg Glu Ile Thr
    290                 295                 300
gag gca gct gtg ctt cta ttc tat cgt tgagagtttt gtgggaggga             960
```

```
Glu Ala Ala Val Leu Leu Phe Tyr Arg
305                 310
acccagacct ctcctcccaa ccatgagatc ccaaggatgg agaacaactt acccagtagc   1020
tagaatgtta atggcagaag agaaaacaat aaatcatatt gactc                   1065

<210> 52
<211> 937
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (177)...(866)

<400> 52
cttttggaga actgcgcttc tctttcggag ggagtgttcg ccgccgccgc ggccgccacc    60
tggagtttct tcagactcca gatttccctg tcaaccacga ggagtccaga gaggaaacgc   120
ggagcggaga caacagtacc tgacgcctct ttcagcccgg gatcgcccca gcaggg       176
atg ggc gac aag atc tgg ctg ccc ttc ccc gtg ctc ctt ctg gcc gct     224
Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala
  1               5                  10                  15
ctg cct ccg gtg ctg ctg cct ggg gcg gcc ggc ttc aca cct tcc ctc     272
Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
             20                  25                  30
gat agc gac ttc acc ttt acc ctt ccc gcc ggc cag aag gag tgc ttc     320
Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
         35                  40                  45
tac cag ccc atg ccc ctg aag gcc tcg ctg gag atc gag tac caa gtt     368
Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
     50                  55                  60
tta gat gga gca gga tta gat att gat ttc cat ctt gcc tct cca gaa     416
Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu
 65                  70                  75                  80
ggc aaa acc tta gtt ttt gaa caa aga aaa tca gat gga gtt cac act     464
Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
                 85                  90                  95
```



```
gta gag act gaa gtt ggt gat tac atg ttc tgc ttt gac aat aca ttc     512
Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe
            100                 105                 110
agc acc att tct gag aag gtg att ttc ttt gaa tta atc ctg gat aat     560
Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn
        115                 120                 125
atg gga gaa cag gca caa gaa caa gaa gat tgg aag aaa tat att act     608
Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr
    130                 135                 140
ggc aca gat ata ttg gat atg aaa ctg gaa gac atc ctg gaa tcc atc     656
Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Glu Ser Ile
145                 150                 155                 160
aac agc atc aag tcc aga cta agc aaa agt ggg cac ata caa att ctg     704
Asn Ser Ile Lys Ser Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu
                165                 170                 175
ctt aga gca ttt gaa gct cgt gat cga aac ata caa gaa agc aac ttt     752
Leu Arg Ala Phe Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe
            180                 185                 190
gat aga gtc aat ttc tgg tct atg gtt aat tta gtg gtc atg gtg gtg     800
Asp Arg Val Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val
        195                 200                 205
gtg tca gcc att caa gtt tat atg ctg aag agt ctg ttt gaa gat aag     848
Val Ser Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys
    210                 215                 220
agg aaa agt aga act taaaactcca aactagagta cgtaacattg aaaaatg        900
Arg Lys Ser Arg Thr
225
aggcataaaa atgcaataaa ctgttacagt caagacc                            937

<210> 53
<211> 1678
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
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```
<222> (56)...(1459)

<400> 53
agcgctcccg aggccgcggg agcctgcaga gaggacagcc ggcctgcgcc gggac          55
atg cgg ccc cag gag ctc ccc agg ctc gcg ttc ccg ttg ctg ctg ttg      103
Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu
  1               5                  10                  15
ctg ttg ctg ctg ctg ccg ccg ccg ccg tgc cct gcc cac agc gcc acg      151
Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr
             20                  25                  30
cgc ttc gac ccc acc tgg gag tcc ctg gac gcc cgc cag ctg ccc gcg      199
Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala
         35                  40                  45
tgg ttt gac cag gcc aag ttc ggc atc ttc atc cac tgg gga gtg ttt      247
Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe
     50                  55                  60
tcc gtg ccc agc ttc ggt agc gag tgg ttc tgg tgg tat tgg caa aag      295
Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys
 65                  70                  75                  80
gaa aag ata ccg aag tat gtg gaa ttt atg aaa gat aat tac cct cct      343
Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro
                 85                  90                  95
agt ttc aaa tat gaa gat ttt gga cca cta ttt aca gca aaa ttt ttt      391
Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe
            100                 105                 110
aat gcc aac cag tgg gca gat att ttt cag gcc tct ggt gcc aaa tac      439
Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr
        115                 120                 125
att gtc tta act tcc aaa cat cat gaa ggc ttt acc ttg tgg ggg tca      487
Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser
    130                 135                 140
gaa tat tcg tgg aac tgg aat gcc ata gat gag ggg ccc aag agg gac      535
Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp
145                 150                 155                 160
att gtc aag gaa ctt gag gta gcc att agg aac aga act gac ctg cgt      583
```



```
Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg
                165                 170                 175
ttt gga ctg tac tat tcc ctt ttt gaa tgg ttt cat ccg ctc ttc ctt      631
Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu
            180                 185                 190
gag gat gaa tcc agt tca ttc cat aag cgg caa ttt cca gtt tct aag      679
Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys
        195                 200                 205
aca ttg cca gag ctc tat gag tta gtg aac aac tat cag cct gag gtt      727
Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val
    210                 215                 220
ctg tgg tcg gat ggt gac gga gga gca ccg gat caa tac tgg aac agc      775
Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser
225                 230                 235                 240
aca ggc ttc ttg gcc tgg tta tat aat gaa agc cca gtt cgg ggc aca      823
Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr
                245                 250                 255
gta gtc acc aat gat cgt tgg gga gct ggt agc atc tgt aag cat ggt      871
Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly
            260                 265                 270
ggc ttc tat acc tgc agt gat cgt tat aac cca gga cat ctt ttg cca      919
Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro
        275                 280                 285
cat aaa tgg gaa aac tgc atg aca ata gac aaa ctg tcc tgg ggc tat      967
His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr
    290                 295                 300
agg agg gaa gct gga atc tct gac tat ctt aca att gaa gaa ttg gtg     1015
Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val
305                 310                 315                 320
aag caa ctt gta gag aca gtt tca tgt gga gga aat ctt ttg atg aat     1063
Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn
                325                 330                 335
att ggg ccc aca cta gat ggc acc att tct gta gtt ttt gag gag cga     1111
Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg
            340                 345                 350
```

```
ctg agg caa atg ggg tcc tgg cta aaa gtc aat gga gaa gct att tat     1159
Leu Arg Gln Met Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr
        355                 360                 365
gaa acc cat acc tgg cga tcc cag aat gac act gtc acc cca gat gtg     1207
Glu Thr His Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val
    370                 375                 380
tgg tac aca tcc aag cct aaa gaa aaa tta gtc tat gcc att ttt ctt     1255
Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu
385                 390                 395                 400
aaa tgg ccc aca tca gga cag ctg ttc ctt ggc cat ccc aaa gct att     1303
Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile
                405                 410                 415
ctg ggg gca aca gag gtg aaa cta ctg ggc cat gga cag cca ctt aac     1351
Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn
            420                 425                 430
tgg att tct ttg gag caa aat ggc att atg gta gaa ctg cca cag cta     1399
Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu
        435                 440                 445
acc att cat cag atg ccg tgt aaa tgg ggc tgg gct cta gcc ctg act     1447
Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr
    450                 455                 460
aat gtg atc taaagtgcag cagagtggct gatgctgcaa gttatgtcta aggc        1500
Asn Val Ile
465
taggaactat caggtgtcta taattgtagc acatggagaa agcaaatgta aaactggata   1560
agaaaattat tttggcagtt cagccctttc ccttttccc actaaatttt ttcttaaatt    1620
acccatgtaa ccattttaac tctccagtgc actttgccat taaagtctct tcacattg     1678

<210> 54
<211> 467
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (114)...(413)
```



```
<400> 54
aggggagggc ggtgctccgc cgcggtggcg gttgctatcg cttcgcagaa cctactcagg    60
cagccagctg agaagagttg agggaaagtg ctgctgctgg gtctgcagac gcg atg      116
                                                           Met
                                                             1
gat aac gtg cag ccg aaa ata aaa cat cgc ccc ttc tgc ttc agt gtg     164
Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser Val
            5                  10                  15
aaa ggc cac gtg aag atg ctg cgg ctg gat att atc aac tca ctg gta     212
Lys Gly His Val Lys Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val
        20                  25                  30
aca aca gta ttc atg ctc atc gta tct gtg ttg gca ctg ata cca gaa     260
Thr Thr Val Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu
    35                  40                  45
acc aca aca ttg aca gtt ggt gga ggg gtg ttt gca ctt gtg aca gca     308
Thr Thr Thr Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala
50                  55                  60                  65
gta tgc tgt ctt gcc gac ggg gcc ctt att tac cgg aag ctt ctg ttc     356
Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe
                70                  75                  80
aat ccc agc ggt cct tac cag caa aag cct gtg cat gaa aaa aaa gaa     404
Asn Pro Ser Gly Pro Tyr Gln Gln Lys Pro Val His Glu Lys Lys Glu
            85                  90                  95
gtt ttg taattttata ttacttttta gtttgatact aagtattaaa                 450
Val Leu

catatttctg tattctt                                                   467

<210> 55
<211> 875
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
```

<222> (272)...(841)

<400> 55

```
attggttggg ggaaacccac gaggggacgc ggccgaggag ggtcgctgtc caccogggg     60
cgtgggagtg aggtaccaga ttcagcccat ttggccccga cgcctctgtt ctcggaatcc   120
gggtgctgcg gattgaggtc ccggttccta acgaatctct gctggattgg ccgtaaccct   180
gtccccgagc gggctcacag ggtctgaagg ccacgcatga ggcaaaggta aagttctgag   240
ccaccoggtg cctccttccc aggactgcaa g atg gag gaa ggc ggg aac cta      292
                                   Met Glu Glu Gly Gly Asn Leu
                                     1               5
gga ggc ctg att aag atg gtc cat cta ctg gtc ttg tca ggt gcc tgg     340
Gly Gly Leu Ile Lys Met Val His Leu Leu Val Leu Ser Gly Ala Trp
         10                  15                  20
ggc atg caa atg tgg gtg acc ttc gtc tca ggc ttc ctg ctt ttc cga     388
Gly Met Gln Met Trp Val Thr Phe Val Ser Gly Phe Leu Leu Phe Arg
     25                  30                  35
agc ctt ccc cga cat acc ttc gga cta gtg cag agc aaa ctc ttc ccc     436
Ser Leu Pro Arg His Thr Phe Gly Leu Val Gln Ser Lys Leu Phe Pro
 40                  45                  50                  55
ttc tac ttc cac atc tcc atg ggc tgt gcc ttc atc aac ctc tgc atc     484
Phe Tyr Phe His Ile Ser Met Gly Cys Ala Phe Ile Asn Leu Cys Ile
                 60                  65                  70
ttg gct tca cag cat gct tgg gct cag ctc aca ttc tgg gag gcc agc     532
Leu Ala Ser Gln His Ala Trp Ala Gln Leu Thr Phe Trp Glu Ala Ser
             75                  80                  85
cag ctt tac ctg ctg ttc ctg agc ctt acg ctg gcc act gtc aac gcc     580
Gln Leu Tyr Leu Leu Phe Leu Ser Leu Thr Leu Ala Thr Val Asn Ala
         90                  95                 100
cgc tgg ctg gaa ccc cgc acc aca gct gcc atg tgg gcc ctg caa acc     628
Arg Trp Leu Glu Pro Arg Thr Thr Ala Ala Met Trp Ala Leu Gln Thr
    105                 110                 115
gtg gag aag gag cga ggc ctg ggt ggg gag gta cca ggc agc cac cag     676
Val Glu Lys Glu Arg Gly Leu Gly Gly Glu Val Pro Gly Ser His Gln
120                 125                 130                 135
ggt ccc gat ccc tac cgc cag ctg cga gag aag gac ccc aag tac agt     724
```



```
Gly Pro Asp Pro Tyr Arg Gln Leu Arg Glu Lys Asp Pro Lys Tyr Ser
                140                 145                 150
gct ctc cgc cag aat ttc ttc cgc tac cat ggg ctg tcc tct ctt tgc     772
Ala Leu Arg Gln Asn Phe Phe Arg Tyr His Gly Leu Ser Ser Leu Cys
            155                 160                 165
aat ctg ggc tgc gtc ctg agc aat ggg ctc tgt ctc gct ggc ctt gcc     820
Asn Leu Gly Cys Val Leu Ser Asn Gly Leu Cys Leu Ala Gly Leu Ala
        170                 175                 180
ctg gaa ata agg agc ctc tagcatgggc cctgcatgct aataaatgct tcttcag   875
Leu Glu Ile Arg Ser Leu
    185
```

<210> 56
<211> 1256
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (150)...(1241)

<400> 56

```
atgtaagagc cacctcctcc ccaggactca gggatggctc tccagatgtc accactgcag    60
atattggagc caacactcca gatgctacaa aaggctgtcc agatgtccaa gcttccttgc   120
cagatgccaa agccaagtcc ccaccgacc atg gtg gac agc ctc ctg gca gtc     173
                                Met Val Asp Ser Leu Leu Ala Val
                                  1               5
acc ctg gct gga aac ctg ggc ctg acc ttc ctc cga ggt tcc cag acc     221
Thr Leu Ala Gly Asn Leu Gly Leu Thr Phe Leu Arg Gly Ser Gln Thr
     10                  15                  20
cag agc cat cca gac ctg gga act gag ggc tgc tgg gac cag ctc tct     269
Gln Ser His Pro Asp Leu Gly Thr Glu Gly Cys Trp Asp Gln Leu Ser
 25                  30                  35                  40
gcc cct cgg acc ttt acg ctt ttg gac ccc aag gca tct ctg tta acc     317
Ala Pro Arg Thr Phe Thr Leu Leu Asp Pro Lys Ala Ser Leu Leu Thr
                 45                  50                  55
```

```
aag gcc ttc ctc aat ggc gcc ctg gat ggg gtc atc ctt gga gac tac      365
Lys Ala Phe Leu Asn Gly Ala Leu Asp Gly Val Ile Leu Gly Asp Tyr
                60                  65                  70
ctg agc cgg act cct gag ccc cgg cca tcc ctc agc cac ttg ctg agc      413
Leu Ser Arg Thr Pro Glu Pro Arg Pro Ser Leu Ser His Leu Leu Ser
            75                  80                  85
cag tac tat ggg gct ggg gtg gcc aga gac cca ggg ttc cgc agc aac      461
Gln Tyr Tyr Gly Ala Gly Val Ala Arg Asp Pro Gly Phe Arg Ser Asn
        90                  95                  100
ttc cga cgg cag aac ggt gct gct ctg act tca gcc tcc atc ctg gcc      509
Phe Arg Arg Gln Asn Gly Ala Ala Leu Thr Ser Ala Ser Ile Leu Ala
105                 110                 115                 120
cag cag gtg tgg gga acc ctt gtc ctt cta cag agg ctg gag cca gta      557
Gln Gln Val Trp Gly Thr Leu Val Leu Leu Gln Arg Leu Glu Pro Val
                125                 130                 135
cac ctc cag ctt cag tgc atg agc caa gaa cag ctg gcc cag gtg gct      605
His Leu Gln Leu Gln Cys Met Ser Gln Glu Gln Leu Ala Gln Val Ala
            140                 145                 150
gcc aat gct acc aag gaa ttc act gag gcc ttc ctg gga tgc ccg gcc      653
Ala Asn Ala Thr Lys Glu Phe Thr Glu Ala Phe Leu Gly Cys Pro Ala
        155                 160                 165
atc cac ccc cgc tgc cgc tgg gga gcg gcg cct tat cgg ggc cgc ccg      701
Ile His Pro Arg Cys Arg Trp Gly Ala Ala Pro Tyr Arg Gly Arg Pro
    170                 175                 180
aag ctg ctg cag ctg ccg ctg gga ttc ttg tac gtg cat cac acc tac      749
Lys Leu Leu Gln Leu Pro Leu Gly Phe Leu Tyr Val His His Thr Tyr
185                 190                 195                 200
gtg cct gca cca ccc tgc acg gac ttc acg cgc tgc gca gcc aac atg      797
Val Pro Ala Pro Pro Cys Thr Asp Phe Thr Arg Cys Ala Ala Asn Met
                205                 210                 215
cgc tcc atg cag cgc tac cac cag gac acg caa ggc tgg gga gac atc      845
Arg Ser Met Gln Arg Tyr His Gln Asp Thr Gln Gly Trp Gly Asp Ile
            220                 225                 230
ggc tac agt ttc gtg gtg ggc tcg gac ggc tac gtg tac gag gga cgc      893
Gly Tyr Ser Phe Val Val Gly Ser Asp Gly Tyr Val Tyr Glu Gly Arg
```



```
        235                 240                 245
ggc tgg cac tgg gtg ggc gcc cac acg ctc ggc cac aac tcc cgg ggc      941
Gly Trp His Trp Val Gly Ala His Thr Leu Gly His Asn Ser Arg Gly
    250                 255                 260
ttc ggc gtg gcc ata gtg ggc aac tac acc gcg gcg ctg ccc acc gag      989
Phe Gly Val Ala Ile Val Gly Asn Tyr Thr Ala Ala Leu Pro Thr Glu
265                 270                 275                 280
gcc gct ctg cgc acg gtg cgc gac acg ctc ccg agt tgt gcg gtg cgc      1037
Ala Ala Leu Arg Thr Val Arg Asp Thr Leu Pro Ser Cys Ala Val Arg
                285                 290                 295
gcc ggc ctc ctg cgg cca gac tac gcg ctg ctg ggc cac cgc cag ctg      1085
Ala Gly Leu Leu Arg Pro Asp Tyr Ala Leu Leu Gly His Arg Gln Leu
            300                 305                 310
gtg cgc acc gac tgc ccc ggc gac gcg ctc ttc gac ctg ctg cgc acc      1133
Val Arg Thr Asp Cys Pro Gly Asp Ala Leu Phe Asp Leu Leu Arg Thr
        315                 320                 325
tgg ccg cac ttc acc gcg act gtt aag cca aga cct gcc agg agt gtc      1181
Trp Pro His Phe Thr Ala Thr Val Lys Pro Arg Pro Ala Arg Ser Val
    330                 335                 340
tct aag aga tcc agg agg gag cca ccc cca agg acc ctg cca gcc aca      1229
Ser Lys Arg Ser Arg Arg Glu Pro Pro Pro Arg Thr Leu Pro Ala Thr
345                 350                 355                 360
gac ctc caa taaagacagc atggaaac                                      1256
Asp Leu Gln

<210> 57
<211> 884
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (135)...(884)

<400> 57
catttccttt ctccacatcc aggtcaggtg gcgtttgctg tggcggctag gcccgcgtgc      60
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gctggagacc tccgcgctgg cccccgcgag cctcctgccc tggcccggcg ctgcggctct 120

gccgcggcgg cagc atg ggt ggc ccc cgg ggc gcg ggc tgg gtg gcg gcg 170

Met Gly Gly Pro Arg Gly Ala Gly Trp Val Ala Ala

1 5 10

ggc ctg ctg ctc ggc gcg ggc gcc tgc tac tgc att tac agg ctg acc 218

Gly Leu Leu Leu Gly Ala Gly Ala Cys Tyr Cys Ile Tyr Arg Leu Thr

15 20 25

cgg ggt cgg cgg cgg ggc gac cgc gag ctc ggg ata cgc tct tcg aag 266

Arg Gly Arg Arg Arg Gly Asp Arg Glu Leu Gly Ile Arg Ser Ser Lys

30 35 40

tcc gca gaa gac tta act gat ggt tca tat gat gat gtt cta aat gct 314

Ser Ala Glu Asp Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala

45 50 55 60

gaa caa ctt cag aaa ctc ctt tac ctg ctg gag tca acg gag gat cct 362

Glu Gln Leu Gln Lys Leu Leu Tyr Leu Leu Glu Ser Thr Glu Asp Pro

65 70 75

gta att att gaa aga gct ttg att act ttg ggt aac aat gca gcc ttt 410

Val Ile Ile Glu Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe

80 85 90

tca gtt aac caa gct att att cgt gaa ttg ggt ggt att cca att gtt 458

Ser Val Asn Gln Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val

95 100 105

gca aac aaa atc aac cat tcc aac cag agt att aaa gag aaa gct tta 506

Ala Asn Lys Ile Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu

110 115 120

aat gca cta aat aac ctg agt gtg aat gtt gaa aat caa atc aag ata 554

Asn Ala Leu Asn Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile

125 130 135 140

aag gtg caa gtt ttg aaa ctg ctt ttg aat ttg tct gaa aat cca gcc 602

Lys Val Gln Val Leu Lys Leu Leu Leu Asn Leu Ser Glu Asn Pro Ala

145 150 155

atg aca gaa gga ctt ctc cgt gcc caa gtg gat tca tca ttc ctt tcc 650

Met Thr Glu Gly Leu Leu Arg Ala Gln Val Asp Ser Ser Phe Leu Ser

160 165 170

ctt tat gac agc cac gta gca aag gag att ctt ctt cga gta ctt acg 698

Leu Tyr Asp Ser His Val Ala Lys Glu Ile Leu Leu Arg Val Leu Thr

175 180 185

cta ttt cag aat ata aag aac tgc ctc aaa ata gaa ggc cat tta gct 746

Leu Phe Gln Asn Ile Lys Asn Cys Leu Lys Ile Glu Gly His Leu Ala

190 195 200

gtg cag cct act ttc act gaa ggt tca ttg ttt ttc ctg tta cat gga 794

Val Gln Pro Thr Phe Thr Glu Gly Ser Leu Phe Phe Leu Leu His Gly

205 210 215 220

gaa gaa tgt gcc cag aaa ata aga gct tta gtt gat cac cat gat gca 842

Glu Glu Cys Ala Gln Lys Ile Arg Ala Leu Val Asp His His Asp Ala

225 230 235

gag gtg aag gaa aag gtt gta aca ata ata ccc aaa atc tga 884

Glu Val Lys Glu Lys Val Val Thr Ile Ile Pro Lys Ile

240 245

<210> 58

<211> 589

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (48)...(344)

<400> 58

gctttccgag cccgcttgca cctcggcgat ccccgactcc cttcttt atg gcg tcg 56

Met Ala Ser

1

ctc ctg tgc tgt ggg ccg aag ctg gcc gcc tgc ggc atc gtc ctc agc 104

Leu Leu Cys Cys Gly Pro Lys Leu Ala Ala Cys Gly Ile Val Leu Ser

5 10 15

gcc tgg gga gtg atc atg ttg ata atg ctc gga ata ttt ttc aat gtc 152

Ala Trp Gly Val Ile Met Leu Ile Met Leu Gly Ile Phe Phe Asn Val

20 25 30 35

cat tcc gct gtg ttg att gag gac gtt ccc ttc acg gag aaa gat ttt 200

His Ser Ala Val Leu Ile Glu Asp Val Pro Phe Thr Glu Lys Asp Phe

```
                40                  45                  50
gag aat ggc ccc cag aac ata tac aac ctt tac gag caa gtc agc tac      248
Glu Asn Gly Pro Gln Asn Ile Tyr Asn Leu Tyr Glu Gln Val Ser Tyr
            55                  60                  65
aac tgt ttc atc gct gca ggc ctt tac ctc ctc ctc gga ggc ttc tct      296
Asn Cys Phe Ile Ala Ala Gly Leu Tyr Leu Leu Leu Gly Gly Phe Ser
        70                  75                  80
ttc tgc caa gtt cgg ctc aat aag cgc aag gaa tac atg gtg cgc          341
Phe Cys Gln Val Arg Leu Asn Lys Arg Lys Glu Tyr Met Val Arg
    85                  90                  95
tagggcccc ggcgcgtttc cccgctccag cccctcctct atttaaagac tccctgcacc     400
gtgtcaccca ggtcgcgtcc caccccttgcc ggcgccctct gtgggactgg gtttcccggg  460
cgagagactg aatcccttct cccatctctg gcatccggcc cccgtggaga gggctgaggc    520
tggggggctg ttccgtctct ccacccttcg ctgtgtcccg tatctcaata aagagaatct    580
gctctcttc                                                            589
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<210> 59
<211> 673
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (25)...(543)

<400> 59

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cttgccttgc gctgcgcgct cacc atg gtg ggc ccc gcg ccg cgg cgg cgg       51
                           Met Val Gly Pro Ala Pro Arg Arg Arg
                             1               5
ctg cgg ccg ctg gca gcg ctg gcc ctg gtc ctg gcg ctg gcc ccg ggg      99
Leu Arg Pro Leu Ala Ala Leu Ala Leu Val Leu Ala Leu Ala Pro Gly
 10                  15                  20                  25
ctg ccc aca gcc cgg gcc ggg cag aca ccg cgc cct gcc gag cgg ggg      147
Leu Pro Thr Ala Arg Ala Gly Gln Thr Pro Arg Pro Ala Glu Arg Gly
                30                  35                  40
ccc cca gtg cgg ctt ttc acc gag gag gag ctg gcc cgc tat ggc ggg      195
```



```
Pro Pro Val Arg Leu Phe Thr Glu Glu Glu Leu Ala Arg Tyr Gly Gly
            45                  50                  55
gag gag gaa gat cag ccc atc tac ttg gca gtg aag gga gtg gtg ttt      243
Glu Glu Glu Asp Gln Pro Ile Tyr Leu Ala Val Lys Gly Val Val Phe
        60                  65                  70
gat gtc acc tcc gga aag gag ttt tat gga cga gga gcc ccc tac aat      291
Asp Val Thr Ser Gly Lys Glu Phe Tyr Gly Arg Gly Ala Pro Tyr Asn
    75                  80                  85
gcc ttg acg ggg aag gac tcc act aga ggg gta gcc aag atg tcc ttg      339
Ala Leu Thr Gly Lys Asp Ser Thr Arg Gly Val Ala Lys Met Ser Leu
 90                  95                 100                 105
gat cct gca gac ctc acc cat gac act acg ggt ctc acg gcc aag gaa      387
Asp Pro Ala Asp Leu Thr His Asp Thr Thr Gly Leu Thr Ala Lys Glu
                110                 115                 120
ctg gag gcc ctg gat gag gtc ttc acc aaa gtg tac aaa gcc aaa tac      435
Leu Glu Ala Leu Asp Glu Val Phe Thr Lys Val Tyr Lys Ala Lys Tyr
            125                 130                 135
ccc atc gtc ggc tac act gcc cgg aga att ctc aat gag gat ggc agc      483
Pro Ile Val Gly Tyr Thr Ala Arg Arg Ile Leu Asn Glu Asp Gly Ser
        140                 145                 150
cct aac ctg gac ttc aag cct gaa gac cag ccc cat ttt gac atc aag      531
Pro Asn Leu Asp Phe Lys Pro Glu Asp Gln Pro His Phe Asp Ile Lys
    155                 160                 165
gat gag ttc tgatgttccc cctgcaggag caggttcttg ggagcgtgag              580
Asp Glu Phe
170
gcaggaagac actaggtgct gaatctcctg caaaactggc tgcctggagg ccctgagcca    640
cccagatctg aataaaacag atgcttaccc tgg                                 673
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<210> 60
<211> 1425
<212> DNA
<213> Homo sapiens
<220>
<221> CDS

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<222> (127)...(489)

<400> 60
tcccgcctgg ggccggctga gtggcactta agcgggccat gccatgcaac cttgggcgct      60
gccaaccgtg ggcgagctct gggtgtgcgg gcggcctggc gcggcgctcc gctgtgtcag     120
cgtgtt atg atg ccg tcc cgt acc aac ctg gct act gga atc ccc agt        168
       Met Met Pro Ser Arg Thr Asn Leu Ala Thr Gly Ile Pro Ser
         1               5                  10
agt aaa gtg aaa tat tca agg ctc tcc agc aca gac gat ggc tac att       216
Ser Lys Val Lys Tyr Ser Arg Leu Ser Ser Thr Asp Asp Gly Tyr Ile
 15                  20                  25                  30
gac ctt cag ttt aag aaa acc cct cct aag atc cct tat aag gcc atc       264
Asp Leu Gln Phe Lys Lys Thr Pro Pro Lys Ile Pro Tyr Lys Ala Ile
                 35                  40                  45
gca ctt gcc act gtg ctg ttt ttg att ggc gcc ttt ctc att att ata       312
Ala Leu Ala Thr Val Leu Phe Leu Ile Gly Ala Phe Leu Ile Ile Ile
             50                  55                  60
ggc tcc ctc ctg ctg tca ggc tac atc agc aaa ggg ggg gca gac cgg       360
Gly Ser Leu Leu Leu Ser Gly Tyr Ile Ser Lys Gly Gly Ala Asp Arg
         65                  70                  75
gcc gtt cca gtg ctg atc att ggc att ctg gtg ttc cta ccc gga ttt       408
Ala Val Pro Val Leu Ile Ile Gly Ile Leu Val Phe Leu Pro Gly Phe
     80                  85                  90
tac cac ctg cgc atc gct tac tat gca tcc aaa ggc tac cgt ggt tac       456
Tyr His Leu Arg Ile Ala Tyr Tyr Ala Ser Lys Gly Tyr Arg Gly Tyr
 95                 100                 105                 110
tcc tat gat gac att cca gac ttt gat gac tagcacccac ccca               500
Ser Tyr Asp Asp Ile Pro Asp Phe Asp Asp
                115                 120
tagctgagga ggagtcacag tggaactgtc ccagctttaa gatatctagc agaaactata     560
gctgaggact aaggaattct gcagcttgca gatgtttaag aaaataatgg ccagattttt     620
tgggtccttc ccaaagatgt taagtgaacc tacagttagc taattaggac aagctctatt     680
tttcatccct gggccctgac aagtttttcc acaggaatat gtatcatgga agaatagagg     740
ttattctgta atggaaaagt gttgcctgcc accaccctct gtagagctga gcatttcttt     800
taaatagtct tcattgccaa tttgttcttg tagcaaatgg aacaatgtgg tatggctaat     860
```



```
ttcttattat taagtagttt attttaaaaa tatctgagta tattatcctg tacacttatc     920
cctaccttca tgttccagtg gaagacctta gtaaaatcaa agatcagtga gttcatctgt     980
aatatttttt ttacttgctt tcttactgac agcaaccagg aatttttta tcctgcagag     1040
caagttttca aaatgtaaat acttcctctg tttaacagtc cttggaccat tctgatccag    1100
ttcaccagta ggttggacag catataattt gcatcatttt gtcccttgta aatcaagatg    1160
ttctgcagat tattccttta acggccggac ttttggctgt ttcctaatga aacatgtagt    1220
ggttattatt tagagtttat agccgtattg ctagcacctt gtagtatgtc atcattctgc    1280
tcatgattcc aaggatcagc ctggatgcct agaggactag atcaccttag tttgattcta    1340
ttttttagct tgcaaaaagt gacttatatt ccaaagaaat taaaatgttg aaatccaaat    1400
cctagaaata aaatgagtta acttc                                          1425

<210> 61
<211> 307
<212> PRT
<213> Homo sapiens

<400> 61
Met Ser Met Ile Leu Ser Ala Ser Val Ile Arg Val Arg Asp Gly Leu
  1               5                  10                  15
Pro Leu Ser Ala Ser Thr Asp Tyr Glu Gln Ser Thr Gly Met Gln Glu
             20                  25                  30
Cys Arg Lys Tyr Phe Lys Met Leu Ser Arg Lys Leu Ala Gln Leu Pro
         35                  40                  45
Asp Arg Cys Thr Leu Lys Thr Gly His Tyr Asn Ile Asn Phe Ile Ser
     50                  55                  60
Ser Leu Gly Val Ser Tyr Met Met Leu Cys Thr Glu Asn Tyr Pro Asn
 65                  70                  75                  80
Val Leu Ala Phe Ser Phe Leu Asp Glu Leu Gln Lys Glu Phe Ile Thr
                 85                  90                  95
Thr Tyr Asn Met Met Lys Thr Asn Thr Ala Val Arg Pro Tyr Cys Phe
            100                 105                 110
Ile Glu Phe Asp Asn Phe Ile Gln Arg Thr Lys Gln Arg Tyr Asn Asn
        115                 120                 125
Pro Arg Ser Leu Ser Thr Lys Ile Asn Leu Ser Asp Met Gln Thr Glu
    130                 135                 140
```

```
Ile Lys Leu Arg Pro Pro Tyr Gln Ile Ser Met Cys Glu Leu Gly Ser
145                 150                 155                 160
Ala Asn Gly Val Thr Ser Ala Phe Ser Val Asp Cys Lys Gly Ala Gly
                165                 170                 175
Lys Ile Ser Ser Ala His Gln Arg Leu Glu Pro Ala Thr Leu Ser Gly
            180                 185                 190
Ile Val Gly Phe Ile Leu Ser Leu Leu Cys Gly Ala Leu Asn Leu Ile
        195                 200                 205
Arg Gly Phe His Ala Ile Glu Ser Leu Leu Gln Ser Asp Gly Asp Asp
    210                 215                 220
Phe Asn Tyr Ile Ile Ala Phe Phe Leu Gly Thr Ala Ala Cys Leu Tyr
225                 230                 235                 240
Gln Cys Tyr Leu Leu Val Tyr Tyr Thr Gly Trp Arg Asn Val Lys Ser
                245                 250                 255
Phe Leu Thr Phe Gly Leu Ile Cys Leu Cys Asn Met Tyr Leu Tyr Glu
            260                 265                 270
Leu Arg Asn Leu Trp Gln Leu Phe Phe His Val Thr Val Gly Ala Phe
        275                 280                 285
Val Thr Leu Gln Ile Trp Leu Arg Gln Ala Gln Gly Lys Ala Pro Asp
    290                 295                 300
Tyr Asp Val
305
```

<210> 62
<211> 183
<212> PRT
<213> Homo sapiens

<400> 62

```
Met Thr Ala Gln Gly Gly Leu Val Ala Asn Arg Gly Arg Arg Phe Lys
1               5                   10                  15
Trp Ala Ile Glu Leu Ser Gly Pro Gly Gly Gly Ser Arg Gly Arg Ser
            20                  25                  30
Asp Arg Gly Ser Gly Gln Gly Asp Ser Leu Tyr Pro Val Gly Tyr Leu
        35                  40                  45
```



```
Asp Lys Gln Val Pro Asp Thr Ser Val Gln Glu Thr Asp Arg Ile Leu
    50                  55                  60
Val Glu Lys Arg Cys Trp Asp Ile Ala Leu Gly Pro Leu Lys Gln Ile
65                  70                  75                  80
Pro Met Asn Leu Phe Ile Met Tyr Met Ala Gly Asn Thr Ile Ser Ile
                85                  90                  95
Phe Pro Thr Met Met Val Cys Met Met Ala Trp Arg Pro Ile Gln Ala
            100                 105                 110
Leu Met Ala Ile Ser Ala Thr Phe Lys Met Leu Glu Ser Ser Ser Gln
        115                 120                 125
Lys Phe Leu Gln Gly Leu Val Tyr Leu Ile Gly Asn Leu Met Gly Leu
    130                 135                 140
Ala Leu Ala Val Tyr Lys Cys Gln Ser Met Gly Leu Leu Pro Thr His
145                 150                 155                 160
Ala Ser Asp Trp Leu Ala Phe Ile Glu Pro Pro Glu Arg Met Glu Phe
            165                 170                 175
Ser Gly Gly Gly Leu Leu Leu
            180
```

<210> 63
<211> 327
<212> PRT
<213> Homo sapiens

<400> 63

```
Met Arg Ala Leu Pro Gly Leu Leu Glu Ala Arg Ala Arg Thr Pro Arg
1               5                   10                  15
Leu Leu Leu Leu Gln Cys Leu Leu Ala Ala Ala Arg Pro Ser Ser Ala
            20                  25                  30
Asp Gly Ser Ala Pro Asp Ser Pro Phe Thr Ser Pro Pro Leu Arg Glu
        35                  40                  45
Glu Ile Met Ala Asn Asn Phe Ser Leu Glu Ser His Asn Ile Ser Leu
    50                  55                  60
Thr Glu His Ser Ser Met Pro Val Glu Lys Asn Ile Thr Leu Glu Arg
65                  70                  75                  80
```

Pro Ser Asn Val Asn Leu Thr Cys Gln Phe Thr Thr Ser Gly Asp Leu
85 90 95
Asn Ala Val Asn Val Thr Trp Lys Lys Asp Gly Glu Gln Leu Glu Asn
100 105 110
Asn Tyr Leu Val Ser Ala Thr Gly Ser Thr Leu Tyr Thr Gln Tyr Arg
115 120 125
Phe Thr Ile Ile Asn Ser Lys Gln Met Gly Ser Tyr Ser Cys Phe Phe
130 135 140
Arg Glu Glu Lys Glu Gln Arg Gly Thr Phe Asn Phe Lys Val Pro Glu
145 150 155 160
Leu His Gly Lys Asn Lys Pro Leu Ile Ser Tyr Val Gly Asp Ser Thr
165 170 175
Val Leu Thr Cys Lys Cys Gln Asn Cys Phe Pro Leu Asn Trp Thr Trp
180 185 190
Tyr Ser Ser Asn Gly Ser Val Lys Val Pro Val Gly Val Gln Met Asn
195 200 205
Lys Tyr Val Ile Asn Gly Thr Tyr Ala Asn Glu Thr Lys Leu Lys Ile
210 215 220
Thr Gln Leu Leu Glu Glu Asp Gly Glu Ser Tyr Trp Cys Arg Ala Leu
225 230 235 240
Phe Gln Leu Gly Glu Ser Glu Glu His Ile Glu Leu Val Val Leu Ser
245 250 255
Tyr Leu Val Pro Leu Lys Pro Phe Leu Val Ile Val Ala Glu Val Ile
260 265 270
Leu Leu Val Ala Thr Ile Leu Leu Cys Glu Lys Tyr Thr Gln Lys Lys
275 280 285
Lys Lys His Ser Asp Glu Gly Lys Glu Phe Glu Gln Ile Glu Gln Leu
290 295 300
Lys Ser Asp Asp Ser Asn Gly Ile Glu Asn Asn Val Pro Arg His Arg
305 310 315 320
Lys Asn Glu Ser Leu Gly Gln
325

<210> 64
<211> 223

<212> PRT
<213> Homo sapiens

<400> 64
Met Lys Phe Val Pro Cys Leu Leu Leu Val Thr Leu Ser Cys Leu Gly
1 5 10 15
Thr Leu Gly Gln Ala Pro Arg Gln Lys Gln Gly Ser Thr Gly Glu Glu
20 25 30
Phe His Phe Gln Thr Gly Gly Arg Asp Ser Cys Thr Met Arg Pro Ser
35 40 45
Ser Leu Gly Gln Gly Ala Gly Glu Val Trp Leu Arg Val Asp Cys Arg
50 55 60
Asn Thr Asp Gln Thr Tyr Trp Cys Glu Tyr Arg Gly Gln Pro Ser Met
65 70 75 80
Cys Gln Ala Phe Ala Ala Asp Pro Lys Ser Tyr Trp Asn Gln Ala Leu
85 90 95
Gln Glu Leu Arg Arg Leu His His Ala Cys Gln Gly Ala Pro Val Leu
100 105 110
Arg Pro Ser Val Cys Arg Glu Ala Gly Pro Gln Ala His Met Gln Gln
115 120 125
Val Thr Ser Ser Leu Lys Gly Ser Pro Glu Pro Asn Gln Gln Pro Glu
130 135 140
Ala Gly Thr Pro Ser Leu Arg Pro Lys Ala Thr Val Lys Leu Thr Glu
145 150 155 160
Ala Thr Gln Leu Gly Lys Asp Ser Met Glu Glu Leu Gly Lys Ala Lys
165 170 175
Pro Thr Thr Arg Pro Thr Ala Lys Pro Thr Gln Pro Gly Pro Arg Pro
180 185 190
Gly Gly Asn Glu Glu Ala Lys Lys Lys Ala Trp Glu His Cys Trp Lys
195 200 205
Pro Phe Gln Ala Leu Cys Ala Phe Leu Ile Ser Phe Phe Arg Gly
210 215 220

<210> 65
<211> 48

<212> PRT
<213> Homo sapiens

<400> 65
Met Arg Leu Leu Leu Leu Leu Leu Val Ala Ala Ser Ala Met Val Arg
1   5   10   15
Ser Glu Ala Ser Ala Asn Leu Gly Gly Val Pro Ser Lys Arg Leu Lys
            20   25   30
Met Gln Tyr Ala Thr Gly Pro Leu Leu Lys Phe Gln Ile Cys Val Ser
        35   40   45

<210> 66
<211> 371
<212> PRT
<213> Homo sapiens

<400> 66
Met Ala Trp Thr Lys Tyr Gln Leu Phe Leu Ala Gly Leu Met Leu Val
1   5   10   15
Thr Gly Ser Ile Asn Thr Leu Ser Ala Lys Trp Ala Asp Asn Phe Met
            20   25   30
Ala Glu Gly Cys Gly Gly Ser Lys Glu His Ser Phe Gln His Pro Phe
        35   40   45
Leu Gln Ala Val Gly Met Phe Leu Gly Glu Phe Ser Cys Leu Ala Ala
    50   55   60
Phe Tyr Leu Leu Arg Cys Arg Ala Ala Gly Gln Ser Asp Ser Ser Val
65   70   75   80
Asp Pro Gln Gln Pro Phe Asn Pro Leu Leu Phe Leu Pro Pro Ala Leu
                85   90   95
Cys Asp Met Thr Gly Thr Ser Leu Met Tyr Val Ala Leu Asn Met Thr
            100   105   110
Ser Ala Ser Ser Phe Gln Met Leu Arg Gly Ala Val Ile Ile Phe Thr
        115   120   125
Gly Leu Phe Ser Val Ala Phe Leu Gly Arg Arg Leu Val Leu Ser Gln
    130   135   140

Trp Leu Gly Ile Leu Ala Thr Ile Ala Gly Leu Val Val Val Gly Leu
145   150   155   160
Ala Asp Leu Leu Ser Lys His Asp Ser Gln His Lys Leu Ser Glu Val
                165   170   175
Ile Thr Gly Asp Leu Leu Ile Ile Met Ala Gln Ile Ile Val Ala Ile
            180   185   190
Gln Met Val Leu Glu Glu Lys Phe Val Tyr Lys His Asn Val His Pro
        195   200   205
Leu Arg Ala Val Gly Thr Glu Gly Leu Phe Gly Phe Val Ile Leu Ser
    210   215   220
Leu Leu Leu Val Pro Met Tyr Tyr Ile Pro Ala Gly Ser Phe Ser Gly
225   230   235   240
Asn Pro Arg Gly Thr Leu Glu Asp Ala Leu Asp Ala Phe Cys Gln Val
                245   250   255
Gly Gln Gln Pro Leu Ile Ala Val Ala Leu Leu Gly Asn Ile Ser Ser
            260   265   270
Ile Ala Phe Phe Asn Phe Ala Gly Ile Ser Val Thr Lys Glu Leu Ser
        275   280   285
Ala Thr Thr Arg Met Val Leu Asp Ser Leu Arg Thr Val Val Ile Trp
    290   295   300
Ala Leu Ser Leu Ala Leu Gly Trp Glu Ala Phe His Ala Leu Gln Ile
305   310   315   320
Leu Gly Phe Leu Ile Leu Leu Ile Gly Thr Ala Leu Tyr Asn Gly Leu
                325   330   335
His Arg Pro Leu Leu Gly Arg Leu Ser Arg Gly Arg Pro Leu Ala Glu
            340   345   350
Glu Ser Glu Gln Glu Arg Leu Leu Gly Gly Thr Arg Thr Pro Ile Asn
        355   360   365
Asp Ala Ser
    370

<210> 67
<211> 90
<212> PRT
<213> Homo sapiens

<400> 67

Met Phe His Gln Ile Trp Ala Ala Leu Leu Tyr Phe Tyr Gly Ile Ile
1 5 10 15
Leu Asn Ser Ile Tyr Gln Cys Pro Glu His Ser Gln Leu Thr Thr Leu
20 25 30
Gly Val Asp Gly Lys Glu Phe Pro Glu Val His Leu Gly Gln Trp Tyr
35 40 45
Phe Ile Ala Gly Ala Ala Pro Thr Lys Glu Glu Leu Ala Thr Phe Asp
50 55 60
Pro Val Asp Asn Ile Val Phe Asn Met Ala Ala Gly Ser Ala Pro Met
65 70 75 80
Gln Leu His Leu Arg Ala Thr Ile Arg Met
85 90

<210> 68
<211> 499
<212> PRT
<213> Homo sapiens

<400> 68

Met Val Asp Arg Gly Pro Leu Leu Thr Ser Ala Ile Ile Phe Tyr Leu
1 5 10 15
Ala Ile Gly Ala Ala Ile Phe Glu Val Leu Glu Glu Pro His Trp Lys
20 25 30
Glu Ala Lys Lys Asn Tyr Tyr Thr Gln Lys Leu His Leu Leu Lys Glu
35 40 45
Phe Pro Cys Leu Gly Gln Glu Gly Leu Asp Lys Ile Leu Glu Val Val
50 55 60
Ser Asp Ala Ala Gly Gln Gly Val Ala Ile Thr Gly Asn Gln Thr Phe
65 70 75 80
Asn Asn Trp Asn Trp Pro Asn Ala Met Ile Phe Ala Ala Thr Val Ile
85 90 95
Thr Thr Ile Gly Tyr Gly Asn Val Ala Pro Lys Thr Pro Ala Gly Arg
100 105 110

Leu Phe Cys Val Phe Tyr Gly Leu Phe Gly Val Pro Leu Cys Leu Thr
115 120 125
Trp Ile Ser Ala Leu Gly Lys Phe Phe Gly Gly Arg Ala Lys Arg Leu
130 135 140
Gly Gln Phe Leu Thr Lys Arg Gly Val Ser Leu Arg Lys Ala Gln Ile
145 150 155 160
Thr Cys Thr Val Ile Phe Ile Val Trp Gly Val Leu Val His Leu Val
165 170 175
Ile Pro Pro Phe Val Phe Met Val Thr Glu Gly Trp Asn Tyr Ile Glu
180 185 190
Gly Leu Tyr Tyr Ser Phe Ile Thr Ile Ser Thr Ile Gly Phe Gly Asp
195 200 205
Phe Val Ala Gly Val Asn Pro Ser Ala Asn Tyr His Ala Leu Tyr Arg
210 215 220
Tyr Phe Val Glu Leu Trp Ile Tyr Leu Gly Leu Ala Trp Leu Ser Leu
225 230 235 240
Phe Val Asn Trp Lys Val Ser Met Phe Val Glu Val His Lys Ala Ile
245 250 255
Lys Lys Arg Arg Arg Arg Arg Lys Glu Ser Phe Glu Ser Ser Pro His
260 265 270
Ser Arg Lys Ala Leu Gln Val Lys Gly Ser Thr Ala Ser Lys Asp Val
275 280 285
Asn Ile Phe Ser Phe Leu Ser Lys Lys Glu Glu Thr Tyr Asn Asp Leu
290 295 300
Ile Lys Gln Ile Gly Lys Lys Ala Met Lys Thr Ser Gly Gly Gly Glu
305 310 315 320
Thr Gly Pro Gly Pro Gly Leu Gly Pro Gln Gly Gly Gly Leu Pro Ala
325 330 335
Leu Pro Pro Ser Leu Val Pro Leu Val Val Tyr Ser Lys Asn Arg Val
340 345 350
Pro Thr Leu Glu Glu Val Ser Gln Thr Leu Arg Ser Lys Gly His Val
355 360 365
Ser Arg Ser Pro Asp Glu Glu Ala Val Ala Arg Ala Pro Glu Asp Ser
370 375 380
Ser Pro Ala Pro Glu Val Phe Met Asn Gln Leu Asp Arg Ile Ser Glu

385 390 395 400
Glu Cys Glu Pro Trp Asp Ala Gln Asp Tyr His Pro Leu Ile Phe Gln
405 410 415
Asp Ala Ser Ile Thr Phe Val Asn Thr Glu Ala Gly Leu Ser Asp Glu
420 425 430
Glu Thr Ser Lys Ser Ser Leu Glu Asp Asn Leu Ala Gly Glu Glu Ser
435 440 445
Pro Gln Gln Gly Ala Glu Ala Lys Ala Pro Leu Asn Met Gly Glu Phe
450 455 460
Pro Ser Ser Ser Glu Ser Thr Phe Thr Ser Thr Glu Ser Glu Leu Ser
465 470 475 480
Val Pro Tyr Glu Gln Leu Met Asn Glu Tyr Asn Lys Ala Asn Ser Pro
485 490 495
Lys Gly Thr

<210> 69
<211> 106
<212> PRT
<213> Homo sapiens

<400> 69
Met Ala Ser Ser Gly Ala Gly Asp Pro Leu Asp Ser Lys Arg Gly Glu
1 5 10 15
Ala Pro Phe Ala Gln Arg Ile Asp Pro Thr Arg Glu Lys Leu Thr Pro
20 25 30
Glu Gln Leu His Ser Met Arg Gln Ala Glu Leu Ala Gln Trp Gln Lys
35 40 45
Val Leu Pro Arg Arg Arg Thr Arg Asn Ile Val Thr Gly Leu Gly Ile
50 55 60
Gly Ala Leu Val Leu Ala Ile Tyr Gly Tyr Thr Phe Tyr Ser Ile Ser
65 70 75 80
Gln Glu Arg Phe Leu Asp Glu Leu Glu Asp Glu Ala Lys Ala Ala Arg
85 90 95
Ala Arg Ala Leu Ala Arg Ala Ser Gly Ser

100 105

<210> 70
<211> 152
<212> PRT
<213> Homo sapiens

<400> 70
Met Asp Tyr Val Cys Cys Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp
1 5 10 15
Glu Thr His Phe Thr Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu
20 25 30
Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly Ile
35 40 45
Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp Lys Lys
50 55 60
Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly Arg Pro Glu
65 70 75 80
Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His Glu Asp Ala Leu
85 90 95
Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe Pro Asp Val Ser Gly
100 105 110
Val Ser Arg Ile Pro Ser Arg Ser Val Pro Ala Ser Asp Cys Val Ser
115 120 125
Gly Gln Asp Leu His Ser Thr Val Tyr Glu Val Ile Gln His Ile Pro
130 135 140
Ala Gln Gln Gln Asp His Pro Glu
145 150

<210> 71
<211> 921
<212> DNA
<213> Homo sapiens

<400> 71

atgtctatga ttttatctgc ctcagtcatt cgtgtcagag atggactgcc actttctgct 60
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tcgaggaaac ttgctcaact tcctgataga tgtacactga aaactggaca ttataacatt 180
aattttatta gctctctggg agtgagctac atgatgttgt gcactgaaaa ttacccaaat 240
gttctcgcct tctctttcct ggatgagctt cagaaggagt tcattactac ttataacatg 300
atgaagacaa atactgctgt cagaccatac tgtttcattg aatttgataa cttcattcag 360
aggaccaagc agcgatataa taatcccagg tctctttcaa caaagataaa tctttctgac 420
atgcagacgg aaatcaagct gaggcctcct tatcaaattt ccatgtgcga actggggtca 480
gccaatggag tcacatcagc atttctgtt gactgtaaag gtgctggtaa gatttcttct 540
gctcaccagc gactggaacc agcaactctg tcagggattg taggatttat ccttagtctt 600
ttatgtggag ctctgaattt aattcgaggc tttcatgcta tagaaagtct cctgcagagt 660
gatggtgatg atttaatta catcattgca tttttccttg gaacagcagc ctgcctttac 720
cagtgttatt tacttgtcta ctacaccggc tggcggaatg tcaaatcttt tttgactttt 780
ggcttaatct gtctatgcaa catgtatctc tatgaactgc gcaacctctg gcagcttttc 840
tttcatgtga ctgtgggagc atttgttaca ctacagatct ggctaaggca agcccagggc 900
aaggctcccg attatgatgt c 921

<210> 72
<211> 549
<212> DNA
<213> Homo sapiens

<400> 72
atgacggccc agggggcct ggtggctaac cgaggccggc gcttcaagtg ggccattgag 60
ctaagcgggc ctggaggagg cagcaggggt cgaagtgacc ggggcagtgg ccagggagac 120
tcgctctacc cagtcggtta cttggacaag caagtgcctg ataccagcgt gcaagagaca 180
gaccggatcc tggtggagaa gcgctgctgg gacatcgcct tgggtcccct caaacagatt 240
cccatgaatc tcttcatcat gtacatggca ggcaatacta tctccatctt ccctactatg 300
atggtgtgta tgatggcctg gcgacccatt caggcactta tggccatttc agccactttc 360
aagatgttag aaagttcaag ccagaagttt cttcagggtt tggtctatct cattgggaac 420
ctgatgggtt tggcattggc tgtttacaag tgccagtcca tgggactgtt acctacacat 480
gcatcggatt ggttagcctt cattgagccc cctgagagaa tggagttcag tggtggagga 540
ctgcttttg 549

<210> 73

<211> 981
<212> DNA
<213> Homo sapiens

<400> 73
atgcgcgccc tccccggcct gctggaggcc agggcgcgta cgccccggct gctcctcctc 60
cagtgccttc tcgctgccgc gcgcccaagc tcggcggacg gcagtgcccc agattcgcct 120
tttacaagtc cacctctcag agaagaaata atggcaaata acttttcctt ggagagtcat 180
aacatatcac tgactgaaca ttctagtatg ccagtagaaa aaaatatcac tttagaaagg 240
ccttctaatg taaatctcac atgccagttc acaacatctg ggatttgaa tgcagtaaat 300
gtgacttgga aaaaagatgg tgaacaactt gagaataatt atcttgtcag tgcaacagga 360
agcaccttgt atacccaata caggttcacc atcattaata gcaaacaaat gggaagttat 420
tcttgtttct ttcgagagga aaaggaacaa aggggaacat ttaatttcaa agtccctgaa 480
cttcatggga aaaacaagcc attgatctct tacgtagggg attctactgt cttgacatgt 540
aaatgtcaaa attgttttcc tttaaattgg acctggtaca gtagtaatgg gagtgtaaag 600
gttcctgttg gtgttcaaat gaataaatat gtgatcaatg gaacatatgc taacgaaaca 660
aagctgaaga taacacaact tttggaggaa gatggggaat cttactggtg ccgtgcacta 720
ttccaattag gcgagagtga agaacacatt gagcttgtgg tgctgagcta tttggtgccc 780
ctcaaaccat ttcttgtaat agtggctgag gtgattcttt tagtggccac cattctgctt 840
tgtgaaaagt acacacaaaa gaaaaagaag cactcagatg aggggaaaga atttgagcag 900
attgaacagc tgaaatcaga tgatagcaat ggtatagaaa ataatgtccc caggcataga 960
aaaaatgagt ctctgggcca g 981

<210> 74
<211> 669
<212> DNA
<213> Homo sapiens

<400> 74
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gccccgaggc aaaagcaagg aagcactggg gaggaattcc atttccagac tggagggaga 120
gattcctgca ctatgcgtcc cagcagcttg ggcaaggtg ctggagaagt ctggcttcgc 180
gtcgactgcc gcaacacaga ccagacctac tggtgtgagt acagggggca gcccagcatg 240
tgccaggctt tcgctgctga ccccaaatct tactggaatc aagccctgca ggagctgagg 300
cgccttcacc atgcgtgcca gggggccccg gtgcttaggc catccgtgtg cagggaggct 360

ggaccccagg cccatatgca gcaggtgact tccagcctca agggcagccc agagcccaac 420
cagcagcctg aggctgggac gccatctctg aggcccaagg ccacagtgaa actcacagaa 480
gcaacacagc tgggaaagga ctcgatggaa gagctgggaa aagccaaacc caccacccga 540
cccacagcca aacctaccca gcctggaccc aggcccggag ggaatgagga agcaaagaag 600
aaggcctggg aacattgttg gaaacccttc caggccctgt gcgcctttct catcagcttc 660
ttccgaggg 669

<210> 75
<211> 144
<212> DNA
<213> Homo sapiens

<400> 75
atgaggcttc tgctgcttct cctagtggcg gcgtctgcga tggtccggag cgaggcctcg 60
gccaatctgg gcggcgtgcc cagcaagaga ttaaagatgc agtacgccac ggggccgctg 120
ctcaagttcc agatttgtgt ttcc 144

<210> 76
<211> 1113
<212> DNA
<213> Homo sapiens

<400> 76
atggcctgga ccaagtacca gctgttcctg gccgggctca tgcttgttac cggctccatc 60
aacacgctct cggcaaaatg ggcggacaat ttcatggccg agggctgtgg agggagcaag 120
gagcacagct tccagcatcc cttcctccag gcagtgggca tgttcctggg agaattctcc 180
tgcctggctg ccttctacct cctccgatgc agagctgcag ggcaatcaga ctccagcgta 240
gacccccagc agcccttcaa ccctcttctt ttcctgcccc cagcgctctg tgacatgaca 300
gggaccagcc tcatgtatgt ggctctgaac atgaccagtg cctccagctt ccagatgctg 360
cggggtgcag tgatcatatt cactggcctg ttctcggtgg ccttcctggg ccggaggctg 420
gtgctgagcc agtggctggg catcctagcc accatcgcgg ggctggtggt cgtgggcctg 480
gctgacctcc tgagcaagca cgacagtcag cacaagctca gcgaagtgat cacaggggac 540
ctgttgatca tcatggccca gatcatcgtt gccatccaga tggtgctaga ggagaagttc 600
gtctacaaac acaatgtgca cccactgcgg gcagttggca ctgagggcct ctttggcttt 660
gtgatcctct ccctgctgct ggtgcccatg tactacatcc ccgccggctc cttcagcgga 720

aaccctcgtg ggacactgga ggatgcattg gacgccttct gccaggtggg ccagcagccg 780
ctcattgccg tggcactgct gggcaacatc agcagcattg ccttcttcaa cttcgcaggc 840
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gttgtcatct gggcactgag cctggcactg ggctgggagg ccttccatgc actgcagatc 960
cttggcttcc tcatactcct tataggcact gccctctaca atgggctaca ccgtccgctg 1020
ctgggccgcc tgtccagggg ccggcccctg gcagaggaga gcgagcagga gagactgctg 1080
ggtggcaccc gcactcccat caatgatgcc agc 1113

<210> 77
<211> 270
<212> DNA
<213> Homo sapiens

<400> 77
atgttccacc aaatttgggc agctctgctc tacttctatg gtattatcct taactccatc 60
taccagtgcc ctgagcacag tcaactgaca actctgggcg tggatgggaa ggagttccca 120
gaggtccact tgggccagtg gtactttatc gcaggggcag ctcccaccaa ggaggagttg 180
gcaacttttg accctgtgga caacattgtc ttcaatatgg ctgctggctc tgccccgatg 240
cagctccacc ttcgtgctac catccgcatg 270

<210> 78
<211> 1497
<212> DNA
<213> Homo sapiens

<400> 78
atggtggacc ggggccctct gctcacctcg gccatcatct tctacctggc catcgggggcg 60
gcgatcttcg aagtgctgga ggagccacac tggaaggagg ccaagaaaaa ctactacaca 120
cagaagctgc atctgctcaa ggagttcccg tgcctgggtc aggagggcct ggacaagatc 180
ctagaggtgg tatctgatgc tgcaggacag ggtgtggcca tcacagggaa ccagaccttc 240
aacaactgga actggcccaa tgcaatgatt tttgcagcga ccgtcattac caccattgga 300
tatggcaatg tggctcccaa gacccccgcc ggtcgcctct tctgtgtttt ctatggtctc 360
ttcggggtgc cgctctgcct gacgtggatc agtgccctgg gcaagttctt cgggggacgt 420
gccaagagac tagggcagtt ccttaccaag agaggtgtga gtctgcggaa ggcgcagatc 480
acgtgcacag tcatcttcat cgtgtggggc gtcctagtcc acctggtgat cccacccttc 540

```
gtattcatgg tgactgaggg gtggaactac atcgagggcc tctactactc cttcatcacc     600
atctccacca tcggcttcgg tgactttgtg gccggtgtga accccagcgc caactacaac     660
gccctgtacc gctacttcgt ggagctctgg atctacttgg ggctggcctg gctgtccctt     720
tttgtcaact ggaaggtgag catgtttgtg gaagtccaca aagccattaa gaagcggcgg     780
cggcgacgga aggagtcctt tgagagctcc ccacactccc ggaaggccct gcaggtgaag     840
gggagcacag cctccaagga cgtcaacatc ttcagctttc tttccaagaa ggaagagacc     900
tacaacgacc tcatcaagca gatcgggaag aaggccatga agacaagcgg gggtggggag     960
acgggcccgg gcccagggct ggggcctcaa ggcggtgggc tcccagcact gccccccttcc   1020
ctggtgcccc tggtagtcta ctccaagaac cgggtgccca ccttggaaga ggtgtcacag    1080
acactgagga gcaaaggcca cgtatcaagg tccccagatg aggaggctgt ggcacgggcc    1140
cctgaagaca gctcccctgc ccccgaggtg ttcatgaacc agctggaccg catcagcgag    1200
gaatgcgagc catgggacgc ccaggactac cacccactca tcttccagga cgccagcatc    1260
accttcgtga acacggaggc tggcctctca gacgaggaga cctccaagtc ctcgctagag    1320
gacaacttgg caggggagga gagcccccag caggggggctg aagccaaggc gcccctgaac   1380
atgggcgagt tcccctcctc ctccgagtcc accttcacca gcactgagtc tgagctctct    1440
gtgccttacg aacagctgat gaatgagtac aacaaggcta acagccccaa gggcaca       1497
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<210> 79
<211> 318
<212> DNA
<213> Homo sapiens

<400> 79

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atggcgtctt cgggagctgg tgaccctctg gattctaagc gtggagaggc cccgttcgct     60
cagcgtatcg acccgactcg ggagaagctg acacccgagc aactgcattc catgcggcag    120
gcggagcttg cccagtggca gaaggtccta ccacggcggc gaacccggaa catcgtgacc    180
ggcctaggca tcggggccct ggtgttggct atttatggtt acaccttcta ctcgatttcc    240
caggagcgtt tcctagatga gctagaagac gaggccaaag ctgcccgagc ccgagctctg    300
gcaagggcgt cagggtcc                                                  318
```

<210> 80
<211> 456
<212> DNA
<213> Homo sapiens

<400> 80

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atggactatg tgtgctgtgc ttacaacaac ataaccggca ggcaagatga aactcatttc     60
acagttatca tcacttccgt aggactggag aagcttgcac agaaaggaaa atcattgtca    120
cctttagcaa gtataactgg aatatcacta tttttgatta tatccatgtg tcttctcttc    180
ctatggaaaa aatatcaacc ctacaaagtt ataaaacaga aactagaagg caggccagaa    240
acagaataca ggaaagctca aacattttca ggccatgaag atgctctgga tgacttcgga    300
atatatgaat ttgttgcttt tccagatgtt tctggtgttt ccaggatccc aagcaggtct    360
gttccagcct ctgattgtgt atcggggcaa gatttgcaca gtacagtgta tgaagttatt    420
cagcacatcc ctgcccagca gcaagaccat ccagag                               456
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<210> 81
<211> 1436
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (66)...(989)

<400> 81

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gcacttcggg gcgcgtcact cggagcggcg ggtcccgtct cgacaggtct tctctgttgg     60
ttgaa atg tct atg att tta tct gcc tca gtc att cgt gtc aga gat        107
      Met Ser Met Ile Leu Ser Ala Ser Val Ile Arg Val Arg Asp
        1               5                  10
gga ctg cca ctt tct gct tct act gat tat gaa caa agc aca gga atg      155
Gly Leu Pro Leu Ser Ala Ser Thr Asp Tyr Glu Gln Ser Thr Gly Met
 15                  20                  25                  30
cag gag tgc aga aag tat ttt aaa atg ctt tcg agg aaa ctt gct caa      203
Gln Glu Cys Arg Lys Tyr Phe Lys Met Leu Ser Arg Lys Leu Ala Gln
                 35                  40                  45
ctt cct gat aga tgt aca ctg aaa act gga cat tat aac att aat ttt      251
Leu Pro Asp Arg Cys Thr Leu Lys Thr Gly His Tyr Asn Ile Asn Phe
             50                  55                  60
att agc tct ctg gga gtg agc tac atg atg ttg tgc act gaa aat tac      299
Ile Ser Ser Leu Gly Val Ser Tyr Met Met Leu Cys Thr Glu Asn Tyr
         65                  70                  75
```

```
cca aat gtt ctc gcc ttc tct ttc ctg gat gag ctt cag aag gag ttc      347
Pro Asn Val Leu Ala Phe Ser Phe Leu Asp Glu Leu Gln Lys Glu Phe
    80                  85                  90
att act act tat aac atg atg aag aca aat act gct gtc aga cca tac      395
Ile Thr Thr Tyr Asn Met Met Lys Thr Asn Thr Ala Val Arg Pro Tyr
 95                 100                 105                 110
tgt ttc att gaa ttt gat aac ttc att cag agg acc aag cag cga tat      443
Cys Phe Ile Glu Phe Asp Asn Phe Ile Gln Arg Thr Lys Gln Arg Tyr
                115                 120                 125
aat aat ccc agg tct ctt tca aca aag ata aat ctt tct gac atg cag      491
Asn Asn Pro Arg Ser Leu Ser Thr Lys Ile Asn Leu Ser Asp Met Gln
            130                 135                 140
acg gaa atc aag ctg agg cct cct tat caa att tcc atg tgc gaa ctg      539
Thr Glu Ile Lys Leu Arg Pro Pro Tyr Gln Ile Ser Met Cys Glu Leu
        145                 150                 155
ggg tca gcc aat gga gtc aca tca gca ttt tct gtt gac tgt aaa ggt      587
Gly Ser Ala Asn Gly Val Thr Ser Ala Phe Ser Val Asp Cys Lys Gly
    160                 165                 170
gct ggt aag att tct tct gct cac cag cga ctg gaa cca gca act ctg      635
Ala Gly Lys Ile Ser Ser Ala His Gln Arg Leu Glu Pro Ala Thr Leu
175                 180                 185                 190
tca ggg att gta gga ttt atc ctt agt ctt tta tgt gga gct ctg aat      683
Ser Gly Ile Val Gly Phe Ile Leu Ser Leu Leu Cys Gly Ala Leu Asn
                195                 200                 205
tta att cga ggc ttt cat gct ata gaa agt ctc ctg cag agt gat ggt      731
Leu Ile Arg Gly Phe His Ala Ile Glu Ser Leu Leu Gln Ser Asp Gly
            210                 215                 220
gat gat ttt aat tac atc att gca ttt ttc ctt gga aca gca gcc tgc      779
Asp Asp Phe Asn Tyr Ile Ile Ala Phe Phe Leu Gly Thr Ala Ala Cys
        225                 230                 235
ctt tac cag tgt tat tta ctt gtc tac tac acc ggc tgg cgg aat gtc      827
Leu Tyr Gln Cys Tyr Leu Leu Val Tyr Tyr Thr Gly Trp Arg Asn Val
    240                 245                 250
aaa tct ttt ttg act ttt ggc tta atc tgt cta tgc aac atg tat ctc      875
Lys Ser Phe Leu Thr Phe Gly Leu Ile Cys Leu Cys Asn Met Tyr Leu
```



```
255                 260                 265                 270
tat gaa ctg cgc aac ctc tgg cag ctt ttc ttt cat gtg act gtg gga      923
Tyr Glu Leu Arg Asn Leu Trp Gln Leu Phe Phe His Val Thr Val Gly
                275                 280                 285
gca ttt gtt aca cta cag atc tgg cta agg caa gcc cag ggc aag gct      971
Ala Phe Val Thr Leu Gln Ile Trp Leu Arg Gln Ala Gln Gly Lys Ala
            290                 295                 300
ccc gat tat gat gtc tgacaccatc cttcagatct attgccttgg cttc           1020
Pro Asp Tyr Asp Val
        305
aggggggataa ggagggaaca tatcataact gcactgtgat gaagaagctg ttccccacag  1080
aggagaagct ctgctttctt tctctccaac tttccttttt taaaatcagc atgatgtgcc   1140
tgtgagcatg gaagagtcct ctcagaagaa tgttggccat gagactatca ttcagaggag   1200
gaggggattt ctctcttcaa ggccataaca gtggaagaac agtcatatgc cattggaagt   1260
cttggccagc agtcctgaat ccttcctgaa gagttcagaa aatagatgtg gtattgctct   1320
gaggaccagg caggaggaac tctacaacct gagtttgcct ttgtgaggca ttagtataga   1380
ccaaataaaa agctgcagaa attggaaagt ttatgtttta aataaatgac tgtgat       1436
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<210> 82
<211> 997
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (87)...(638)

<400> 82

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cgaggctata ggacgcagct gttgcc atg acg gcc cag ggg ggc ctg gtg        110
                             Met Thr Ala Gln Gly Gly Leu Val
                               1               5
gct aac cga ggc cgg cgc ttc aag tgg gcc att gag cta agc ggg cct     158
Ala Asn Arg Gly Arg Arg Phe Lys Trp Ala Ile Glu Leu Ser Gly Pro
     10                  15                  20
gga gga ggc agc agg ggt cga agt gac cgg ggc agt ggc cag gga gac     206
```

```
Gly Gly Gly Ser Arg Gly Arg Ser Asp Arg Gly Ser Gly Gln Gly Asp
 25                  30                  35                  40
tcg ctc tac cca gtc ggt tac ttg gac aag caa gtg cct gat acc agc      254
Ser Leu Tyr Pro Val Gly Tyr Leu Asp Lys Gln Val Pro Asp Thr Ser
                 45                  50                  55
gtg caa gag aca gac cgg atc ctg gtg gag aag cgc tgc tgg gac atc      302
Val Gln Glu Thr Asp Arg Ile Leu Val Glu Lys Arg Cys Trp Asp Ile
             60                  65                  70
gcc ttg ggt ccc ctc aaa cag att ccc atg aat ctc ttc atc atg tac      350
Ala Leu Gly Pro Leu Lys Gln Ile Pro Met Asn Leu Phe Ile Met Tyr
         75                  80                  85
atg gca ggc aat act atc tcc atc ttc cct act atg atg gtg tgt atg      398
Met Ala Gly Asn Thr Ile Ser Ile Phe Pro Thr Met Met Val Cys Met
     90                  95                 100
atg gcc tgg cga ccc att cag gca ctt atg gcc att tca gcc act ttc      446
Met Ala Trp Arg Pro Ile Gln Ala Leu Met Ala Ile Ser Ala Thr Phe
105                 110                 115                 120
aag atg tta gaa agt tca agc cag aag ttt ctt cag ggt ttg gtc tat      494
Lys Met Leu Glu Ser Ser Ser Gln Lys Phe Leu Gln Gly Leu Val Tyr
                125                 130                 135
ctc att ggg aac ctg atg ggt ttg gca ttg gct gtt tac aag tgc cag      542
Leu Ile Gly Asn Leu Met Gly Leu Ala Leu Ala Val Tyr Lys Cys Gln
            140                 145                 150
tcc atg gga ctg tta cct aca cat gca tcg gat tgg tta gcc ttc att      590
Ser Met Gly Leu Leu Pro Thr His Ala Ser Asp Trp Leu Ala Phe Ile
        155                 160                 165
gag ccc cct gag aga atg gag ttc agt ggt gga gga ctg ctt ttg tgaac    640
Glu Pro Pro Glu Arg Met Glu Phe Ser Gly Gly Gly Leu Leu Leu
    170                 175                 180
atgagaaagc agcgcctggt ccctatgtat ttgggtctta tttacatcct tctttaagcc    700
cagtggctcc tcagcatact cttaaactaa tcacttatgt taaaaagaac caaaagactc    760
ttttctccat ggtggggtga caggtcctag aaggacaatg tgcatattac gacaaacaca    820
aagaaactat accataaccc aaggctgaaa ataatgtaga aaactttatt tttgtttcca    880
gtacagagca aaacaacaac aaaaaaacat aactatgtaa acaagagaat aactgctgct    940
aaatcaagaa ctgttgcagc atctcctttc aataaattaa atggttgaga acaatgc       997
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<210> 83
<211> 1753
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (134)...(1117)

<400> 83
tcttcagcgt cctacccgcg gcactggctg cgagcgccgg gccacctgcg agtgtgcgca    60
gggactctgg acacccgcgg cggcgagctg agggagcagt ctccacgagg acccaggcgg   120
accctctggc gcc atg cgc gcc ctc ccc ggc ctg ctg gag gcc agg gcg      169
               Met Arg Ala Leu Pro Gly Leu Leu Glu Ala Arg Ala
                 1               5                  10
cgt acg ccc cgg ctg ctc ctc ctc cag tgc ctt ctc gct gcc gcg cgc     217
Arg Thr Pro Arg Leu Leu Leu Leu Gln Cys Leu Leu Ala Ala Ala Arg
         15                  20                  25
cca agc tcg gcg gac ggc agt gcc cca gat tcg cct ttt aca agt cca     265
Pro Ser Ser Ala Asp Gly Ser Ala Pro Asp Ser Pro Phe Thr Ser Pro
     30                  35                  40
cct ctc aga gaa gaa ata atg gca aat aac ttt tcc ttg gag agt cat     313
Pro Leu Arg Glu Glu Ile Met Ala Asn Asn Phe Ser Leu Glu Ser His
 45                  50                  55                  60
aac ata tca ctg act gaa cat tct agt atg cca gta gaa aaa aat atc     361
Asn Ile Ser Leu Thr Glu His Ser Ser Met Pro Val Glu Lys Asn Ile
                 65                  70                  75
act tta gaa agg cct tct aat gta aat ctc aca tgc cag ttc aca aca     409
Thr Leu Glu Arg Pro Ser Asn Val Asn Leu Thr Cys Gln Phe Thr Thr
             80                  85                  90
tct ggg gat ttg aat gca gta aat gtg act tgg aaa aaa gat ggt gaa     457
Ser Gly Asp Leu Asn Ala Val Asn Val Thr Trp Lys Lys Asp Gly Glu
         95                 100                 105
caa ctt gag aat aat tat ctt gtc agt gca aca gga agc acc ttg tat     505
Gln Leu Glu Asn Asn Tyr Leu Val Ser Ala Thr Gly Ser Thr Leu Tyr
```

```
110                 115                 120
acc caa tac agg ttc acc atc att aat agc aaa caa atg gga agt tat      553
Thr Gln Tyr Arg Phe Thr Ile Ile Asn Ser Lys Gln Met Gly Ser Tyr
125                 130                 135                 140
tct tgt ttc ttt cga gag gaa aag gaa caa agg gga aca ttt aat ttc      601
Ser Cys Phe Phe Arg Glu Glu Lys Glu Gln Arg Gly Thr Phe Asn Phe
                145                 150                 155
aaa gtc cct gaa ctt cat ggg aaa aac aag cca ttg atc tct tac gta      649
Lys Val Pro Glu Leu His Gly Lys Asn Lys Pro Leu Ile Ser Tyr Val
            160                 165                 170
ggg gat tct act gtc ttg aca tgt aaa tgt caa aat tgt ttt cct tta      697
Gly Asp Ser Thr Val Leu Thr Cys Lys Cys Gln Asn Cys Phe Pro Leu
        175                 180                 185
aat tgg acc tgg tac agt agt aat ggg agt gta aag gtt cct gtt ggt      745
Asn Trp Thr Trp Tyr Ser Ser Asn Gly Ser Val Lys Val Pro Val Gly
    190                 195                 200
gtt caa atg aat aaa tat gtg atc aat gga aca tat gct aac gaa aca      793
Val Gln Met Asn Lys Tyr Val Ile Asn Gly Thr Tyr Ala Asn Glu Thr
205                 210                 215                 220
aag ctg aag ata aca caa ctt ttg gag gaa gat ggg gaa tct tac tgg      841
Lys Leu Lys Ile Thr Gln Leu Leu Glu Glu Asp Gly Glu Ser Tyr Trp
                225                 230                 235
tgc cgt gca cta ttc caa tta ggc gag agt gaa gaa cac att gag ctt      889
Cys Arg Ala Leu Phe Gln Leu Gly Glu Ser Glu Glu His Ile Glu Leu
            240                 245                 250
gtg gtg ctg agc tat ttg gtg ccc ctc aaa cca ttt ctt gta ata gtg      937
Val Val Leu Ser Tyr Leu Val Pro Leu Lys Pro Phe Leu Val Ile Val
        255                 260                 265
gct gag gtg att ctt tta gtg gcc acc att ctg ctt tgt gaa aag tac      985
Ala Glu Val Ile Leu Leu Val Ala Thr Ile Leu Leu Cys Glu Lys Tyr
    270                 275                 280
aca caa aag aaa aag aag cac tca gat gag ggg aaa gaa ttt gag cag     1033
Thr Gln Lys Lys Lys Lys His Ser Asp Glu Gly Lys Glu Phe Glu Gln
285                 290                 295                 300
att gaa cag ctg aaa tca gat gat agc aat ggt ata gaa aat aat gtc     1081
```



```
Ile Glu Gln Leu Lys Ser Asp Asp Ser Asn Gly Ile Glu Asn Asn Val
                305                 310                 315
ccc agg cat aga aaa aat gag tct ctg ggc cag tgaatacaaa acatca       1130
Pro Arg His Arg Lys Asn Glu Ser Leu Gly Gln
            320                 325
tgtcgagaat cattggaaga tatacagagt tcgtatttca gctttattta tccttcctgt   1190
taagagcctc tgagtttta gttttaaaag gatgaaagc ttatgcaaca tgctcagcag      1250
gagcttcatc aacgatatat gtcagatcta aaggtatatt ttcattctgt aattatgtta   1310
cataaaagca atgtaaatca gaataaatat gttagaccag aataaaatta attatattct   1370
ggtcttcaaa ggacacacag aacagatatc agcagaatca cttaatactt catagaacaa   1430
aaatcactca aaacctgttt ataaccaaag aattcatgaa aaagaaagcc tttgccattt   1490
gtcttagaaa gttatttttt taaaaaaaat catacttact attagtatct atggaagtat   1550
atgtaacaat ttttatgtaa aggtcatctt tctgtgatag tgaaaaaata tgtctttact   1610
aagttgaaat gaatactttc tgcctttgct catgatagtt attctacaat ctccacaaga   1670
aaaatatacc ttttatccgg aaatattggt ttaaggcaaa taaataaaac tgtgcttgct   1730
ctaaagctct gcactacaaa agc                                           1753

&lt;210&gt; 84
&lt;211&gt; 1117
&lt;212&gt; DNA
&lt;213&gt; Homo sapiens
&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; (62)...(733)

&lt;400&gt; 84
cgtcccactt gtgttctctc tcctggtgca gagttgcaag caagtttatc ggagtatcgc     60
c atg aag ttc gtc ccc tgc ctc ctg ctg gtg acc ttg tcc tgc ctg         106
  Met Lys Phe Val Pro Cys Leu Leu Leu Val Thr Leu Ser Cys Leu
  1               5                   10                  15
ggg act ttg ggt cag gcc ccg agg caa aag caa gga agc act ggg gag       154
Gly Thr Leu Gly Gln Ala Pro Arg Gln Lys Gln Gly Ser Thr Gly Glu
                20                  25                  30
gaa ttc cat ttc cag act gga ggg aga gat tcc tgc act atg cgt ccc       202
Glu Phe His Phe Gln Thr Gly Gly Arg Asp Ser Cys Thr Met Arg Pro
```

```
                35                       40                       45
agc agc ttg ggg caa ggt gct gga gaa gtc tgg ctt cgc gtc gac tgc        250
Ser Ser Leu Gly Gln Gly Ala Gly Glu Val Trp Leu Arg Val Asp Cys
            50                       55                       60
cgc aac aca gac cag acc tac tgg tgt gag tac agg ggg cag ccc agc        298
Arg Asn Thr Asp Gln Thr Tyr Trp Cys Glu Tyr Arg Gly Gln Pro Ser
        65                       70                       75
atg tgc cag gct ttc gct gct gac ccc aaa tct tac tgg aat caa gcc        346
Met Cys Gln Ala Phe Ala Ala Asp Pro Lys Ser Tyr Trp Asn Gln Ala
    80                       85                       90                       95
ctg cag gag ctg agg cgc ctt cac cat gcg tgc cag ggg gcc ccg gtg        394
Leu Gln Glu Leu Arg Arg Leu His His Ala Cys Gln Gly Ala Pro Val
                100                      105                      110
ctt agg cca tcc gtg tgc agg gag gct gga ccc cag gcc cat atg cag        442
Leu Arg Pro Ser Val Cys Arg Glu Ala Gly Pro Gln Ala His Met Gln
            115                      120                      125
cag gtg act tcc agc ctc aag ggc agc cca gag ccc aac cag cag cct        490
Gln Val Thr Ser Ser Leu Lys Gly Ser Pro Glu Pro Asn Gln Gln Pro
        130                      135                      140
gag gct ggg acg cca tct ctg agg ccc aag gcc aca gtg aaa ctc aca        538
Glu Ala Gly Thr Pro Ser Leu Arg Pro Lys Ala Thr Val Lys Leu Thr
    145                      150                      155
gaa gca aca cag ctg gga aag gac tcg atg gaa gag ctg gga aaa gcc        586
Glu Ala Thr Gln Leu Gly Lys Asp Ser Met Glu Glu Leu Gly Lys Ala
160                      165                      170                      175
aaa ccc acc acc cga ccc aca gcc aaa cct acc cag cct gga ccc agg        634
Lys Pro Thr Thr Arg Pro Thr Ala Lys Pro Thr Gln Pro Gly Pro Arg
                180                      185                      190
ccc gga ggg aat gag gaa gca aag aag aag gcc tgg gaa cat tgt tgg        682
Pro Gly Gly Asn Glu Glu Ala Lys Lys Lys Ala Trp Glu His Cys Trp
            195                      200                      205
aaa ccc ttc cag gcc ctg tgc gcc ttt ctc atc agc ttc ttc cga ggg        730
Lys Pro Phe Gln Ala Leu Cys Ala Phe Leu Ile Ser Phe Phe Arg Gly
        210                      215                      220
tgacaggtga aagaccccta cagatctgac ctctccctga cagacaacca tctcttttta      790
```



```
tattatgccg ctttcaatcc aacgttctca cactggaaga agagagtttc taatcagatg      850
caacggccca aattcttgat ctgcagcttc tctgaagttt ggaaaagaaa ccttcctttc      910
tggagtttgc agagttcagc aatatgatag ggaacaggtg ctgatgggcc caagagtgac      970
aagcatacac aactacttat tatctgtaga agttttgctt tgttgatctg agccttctat     1030
gaaagtttaa atatgtaacg cattcatgaa tttccagtgt tcagtaaata gcagctatgt     1090
gtgtgcaaaa taaaagaatg atttcag                                         1117
```

<210> 85
<211> 1380
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (43)...(189)

<400> 85

```
gcagtctgtc tgagggcggc cgaagtggct ggctcattta ag atg agg ctt ctg          54
                                               Met Arg Leu Leu
                                                 1
ctg ctt ctc cta gtg gcg gcg tct gcg atg gtc cgg agc gag gcc tcg        102
Leu Leu Leu Leu Val Ala Ala Ser Ala Met Val Arg Ser Glu Ala Ser
  5                       10                       15                       20
gcc aat ctg ggc ggc gtg ccc agc aag aga tta aag atg cag tac gcc        150
Ala Asn Leu Gly Gly Val Pro Ser Lys Arg Leu Lys Met Gln Tyr Ala
                25                       30                       35
acg ggg ccg ctg ctc aag ttc cag att tgt gtt tcc tgag                   190
Thr Gly Pro Leu Leu Lys Phe Gln Ile Cys Val Ser
            40                       45
gttataggcg ggtgtttgag gagtacatgc gggttattag ccagcggtac ccagacatcc      250
gcattgaagg agagaattac ctccctcaac caatatatag acacatagca tctttcctgt      310
cagtcttcaa actagtatta ataggcttaa taattgttgg caaggatcct tttgctttct      370
ttggcatgca agctcctagc atctggcagt ggggccaaga aaataaggtt tatgcatgta      430
tgatggtttt cttcttgagc aacatgattg agaaccagtg tatgtcaaca ggtgcatttg      490
agataacttt aaatgatgta cctgtgtggt ctaagctgga atctggtcac cttccatcca      550
tgcaacaact tgttcaaatt cttgacaatg aaatgaagct caatgtgcat atggattcaa      610
```

```
tcccacacca tcgatcatag caccacctat cagcactgaa aactcttttg cattaaggga    670
tcattgcaag agcagcgtga ctgacattat gaaggcctgt actgaagaca gcaagctgtt    730
agtacagacc agatgctttc ttggcaggct cgttgtacct cttggaaaac ctcaatgcaa    790
gatagtgttt cagtgctggc atattttgga attctgcaca ttcatggagt gcaataatac    850
tgtatagctt tccccacctc ccacaaaatc acccagttaa tgtgtgtgtg tgttttttttt    910
tttaaggtaa acattactac ttgtaacttt ttttcttagt catatttgaa aaagtagaaa    970
attgagttac aatttgattt tttttccaaa gatgtctgtt aaatctgttg tgcttttata   1030
tgaatatttg ttttttatag tttaaaattg atcctttggg aatccagttg aagttcccaa   1090
atactttata agagtttatc agacatctct aatttggcca tgtccagttt atacagttta   1150
caaaatatag cagatgcaag attatggggg aaatcctata ttcagagtac tctataaatt   1210
tttgtgtatg tgtgtatgtg cgtgtgatta ccagagaact actaaaaaaa ccaactgctt   1270
tttaaatcct attgtgtagt taaagtgtca tgccttgacc aatctaatga attgattaat   1330
taactgggcc tttatactta actaaataaa aaactaagca gatatgagtt              1380
```

<210> 86
<211> 1503
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (51)...(1166)

<400> 86

```
gtgacggggc ccggcgccgc taactggagc gaaccccagc gtccgccgac atg gcc      56
                                                      Met Ala
                                                        1
tgg acc aag tac cag ctg ttc ctg gcc ggg ctc atg ctt gtt acc ggc    104
Trp Thr Lys Tyr Gln Leu Phe Leu Ala Gly Leu Met Leu Val Thr Gly
            5                  10                  15
tcc atc aac acg ctc tcg gca aaa tgg gcg gac aat ttc atg gcc gag    152
Ser Ile Asn Thr Leu Ser Ala Lys Trp Ala Asp Asn Phe Met Ala Glu
        20                  25                  30
ggc tgt gga ggg agc aag gag cac agc ttc cag cat ccc ttc ctc cag    200
Gly Cys Gly Gly Ser Lys Glu His Ser Phe Gln His Pro Phe Leu Gln
    35                  40                  45                  50
```



```
gca gtg ggc atg ttc ctg gga gaa ttc tcc tgc ctg gct gcc ttc tac    248
Ala Val Gly Met Phe Leu Gly Glu Phe Ser Cys Leu Ala Ala Phe Tyr
                55                  60                  65
ctc ctc cga tgc aga gct gca ggg caa tca gac tcc agc gta gac ccc    296
Leu Leu Arg Cys Arg Ala Ala Gly Gln Ser Asp Ser Ser Val Asp Pro
            70                  75                  80
cag cag ccc ttc aac cct ctt ctt ttc ctg ccc cca gcg ctc tgt gac    344
Gln Gln Pro Phe Asn Pro Leu Leu Phe Leu Pro Pro Ala Leu Cys Asp
        85                  90                  95
atg aca ggg acc agc ctc atg tat gtg gct ctg aac atg acc agt gcc    392
Met Thr Gly Thr Ser Leu Met Tyr Val Ala Leu Asn Met Thr Ser Ala
    100                 105                 110
tcc agc ttc cag atg ctg cgg ggt gca gtg atc ata ttc act ggc ctg    440
Ser Ser Phe Gln Met Leu Arg Gly Ala Val Ile Ile Phe Thr Gly Leu
115                 120                 125                 130
ttc tcg gtg gcc ttc ctg ggc cgg agg ctg gtg ctg agc cag tgg ctg    488
Phe Ser Val Ala Phe Leu Gly Arg Arg Leu Val Leu Ser Gln Trp Leu
                135                 140                 145
ggc atc cta gcc acc atc gcg ggg ctg gtg gtc gtg ggc ctg gct gac    536
Gly Ile Leu Ala Thr Ile Ala Gly Leu Val Val Val Gly Leu Ala Asp
            150                 155                 160
ctc ctg agc aag cac gac agt cag cac aag ctc agc gaa gtg atc aca    584
Leu Leu Ser Lys His Asp Ser Gln His Lys Leu Ser Glu Val Ile Thr
        165                 170                 175
ggg gac ctg ttg atc atc atg gcc cag atc atc gtt gcc atc cag atg    632
Gly Asp Leu Leu Ile Ile Met Ala Gln Ile Ile Val Ala Ile Gln Met
    180                 185                 190
gtg cta gag gag aag ttc gtc tac aaa cac aat gtg cac cca ctg cgg    680
Val Leu Glu Glu Lys Phe Val Tyr Lys His Asn Val His Pro Leu Arg
195                 200                 205                 210
gca gtt ggc act gag ggc ctc ttt ggc ttt gtg atc ctc tcc ctg ctg    728
Ala Val Gly Thr Glu Gly Leu Phe Gly Phe Val Ile Leu Ser Leu Leu
                215                 220                 225
ctg gtg ccc atg tac tac atc ccc gcc ggc tcc ttc agc gga aac cct    776
Leu Val Pro Met Tyr Tyr Ile Pro Ala Gly Ser Phe Ser Gly Asn Pro
```

230 235 240
cgt ggg aca ctg gag gat gca ttg gac gcc ttc tgc cag gtg ggc cag 824
Arg Gly Thr Leu Glu Asp Ala Leu Asp Ala Phe Cys Gln Val Gly Gln
245 250 255
cag ccg ctc att gcc gtg gca ctg ctg ggc aac atc agc agc att gcc 872
Gln Pro Leu Ile Ala Val Ala Leu Leu Gly Asn Ile Ser Ser Ile Ala
260 265 270
ttc ttc aac ttc gca ggc atc agc gtc acc aag gaa ctg agc gcc acc 920
Phe Phe Asn Phe Ala Gly Ile Ser Val Thr Lys Glu Leu Ser Ala Thr
275 280 285 290
acc cgc atg gtg ttg gac agc ttg cgc acc gtt gtc atc tgg gca ctg 968
Thr Arg Met Val Leu Asp Ser Leu Arg Thr Val Val Ile Trp Ala Leu
295 300 305
agc ctg gca ctg ggc tgg gag gcc ttc cat gca ctg cag atc ctt ggc 1016
Ser Leu Ala Leu Gly Trp Glu Ala Phe His Ala Leu Gln Ile Leu Gly
310 315 320
ttc ctc ata ctc ctt ata ggc act gcc ctc tac aat ggg cta cac cgt 1064
Phe Leu Ile Leu Leu Ile Gly Thr Ala Leu Tyr Asn Gly Leu His Arg
325 330 335
ccg ctg ctg ggc cgc ctg tcc agg ggc cgg ccc ctg gca gag gag agc 1112
Pro Leu Leu Gly Arg Leu Ser Arg Gly Arg Pro Leu Ala Glu Glu Ser
340 345 350
gag cag gag aga ctg ctg ggt ggc acc cgc act ccc atc aat gat gcc 1160
Glu Gln Glu Arg Leu Leu Gly Gly Thr Arg Thr Pro Ile Asn Asp Ala
355 360 365 370
agc tgaggttccc tggaggcttc tactgccacc cgggtgctcc ttctccc 1210
Ser

tgagactgag gccacacagg ctggtgggcc ccgaatgccc tatccccaag gcctcaccct 1270
gtcccctccc tgcagaaccc ccagggcagc tgctgccaca gaagataaca acacccaagt 1330
cctcttttc tcactaccac ctgcagggtg gtgttaccca gcccccacaa gcctgagtgc 1390
agtggcagac ctcagctctc tggaccctc ctacagcact agagctaaat catgaagttg 1450
aattgtagga atttaccacc gtagtgtatc tgaatcataa actagattat cat 1503

<210> 87

<211> 733
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (40)...(312)

<400> 87
gttaaggcac acagagcacc agctccctcc tgcctgaag atg ttc cac caa att 54
Met Phe His Gln Ile
1 5
tgg gca gct ctg ctc tac ttc tat ggt att atc ctt aac tcc atc tac 102
Trp Ala Ala Leu Leu Tyr Phe Tyr Gly Ile Ile Leu Asn Ser Ile Tyr
10 15 20
cag tgc cct gag cac agt caa ctg aca act ctg ggc gtg gat ggg aag 150
Gln Cys Pro Glu His Ser Gln Leu Thr Thr Leu Gly Val Asp Gly Lys
25 30 35
gag ttc cca gag gtc cac ttg ggc cag tgg tac ttt atc gca ggg gca 198
Glu Phe Pro Glu Val His Leu Gly Gln Trp Tyr Phe Ile Ala Gly Ala
40 45 50
gct ccc acc aag gag gag ttg gca act ttt gac cct gtg gac aac att 246
Ala Pro Thr Lys Glu Glu Leu Ala Thr Phe Asp Pro Val Asp Asn Ile
55 60 65
gtc ttc aat atg gct gct ggc tct gcc ccg atg cag ctc cac ctt cgt 294
Val Phe Asn Met Ala Ala Gly Ser Ala Pro Met Gln Leu His Leu Arg
70 75 80 85
gct acc atc cgc atg tgagtggaaa gatgggctct gtgtgccccg g 340
Ala Thr Ile Arg Met
90
aaatggatct accacctgac tgaagggagc acagatctca gaactgaagg ccgccctgac 400
atgaagactg agctctttc cagctcatgc ccaggtggaa tcatgctgaa tgagacaggc 460
cagggttacc agcgctttct cctctacaat cgctcaccac atcctcccga aaagtgtgtg 520
gaggaattca agtccctgac ttcctgcctg gactccaaag ccttcttatt gactcctagg 580
aatcaagagg cctgtgagct gtccaataac tgacctgtaa cttcatctaa gtccccagat 640
gggtacaatg ggagctgagt tgttggaggg agaagctgga gacttccagc tccagctccc 700

```
actcaagata ataaagataa tttttcaatc ctc                               733

<210> 88
<211> 3768
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (358)...(1857)

<400> 88
gctagtggcg cgcggaggag cgacgcgtgg agaagcggcc cacgtgtctg cccagagtca     60
agtcctgtgt tcttcccgct ccttacgcat ccgcggtcca gggcgccctt tcagccccgc    120
tggtgttcgc ccaccccggg ccgcgtgagt ggggccccac gcagctcccc gcactccgtg    180
ggccaacttg gccaagcaac tctgtccggg gagcggtgct tgcggggggt gagtaccggg    240
cactgcgcat gcggagctcc aaattcaaac agctgttttc agaggctgga gggcgggcgg    300
actggtagca gctggggcta ggagaggctt tctctaggag gcggccgctc gggagcc       357


atg gtg gac cgg ggc cct ctg ctc acc tcg gcc atc atc ttc tac ctg      405
Met Val Asp Arg Gly Pro Leu Leu Thr Ser Ala Ile Ile Phe Tyr Leu
  1               5                  10                  15
gcc atc ggg gcg gcg atc ttc gaa gtg ctg gag gag cca cac tgg aag      453
Ala Ile Gly Ala Ala Ile Phe Glu Val Leu Glu Glu Pro His Trp Lys
             20                  25                  30
gag gcc aag aaa aac tac tac aca cag aag ctg cat ctg ctc aag gag      501
Glu Ala Lys Lys Asn Tyr Tyr Thr Gln Lys Leu His Leu Leu Lys Glu
         35                  40                  45
ttc ccg tgc ctg ggt cag gag ggc ctg gac aag atc cta gag gtg gta      549
Phe Pro Cys Leu Gly Gln Glu Gly Leu Asp Lys Ile Leu Glu Val Val
     50                  55                  60
tct gat gct gca gga cag ggt gtg gcc atc aca ggg aac cag acc ttc      597
Ser Asp Ala Ala Gly Gln Gly Val Ala Ile Thr Gly Asn Gln Thr Phe
 65                  70                  75                  80
aac aac tgg aac tgg ccc aat gca atg att ttt gca gcg acc gtc att      645
```



```
Asn Asn Trp Asn Trp Pro Asn Ala Met Ile Phe Ala Ala Thr Val Ile
                 85                  90                  95
acc acc att gga tat ggc aat gtg gct ccc aag acc ccc gcc ggt cgc      693
Thr Thr Ile Gly Tyr Gly Asn Val Ala Pro Lys Thr Pro Ala Gly Arg
            100                 105                 110
ctc ttc tgt gtt ttc tat ggt ctc ttc ggg gtg ccg ctc tgc ctg acg      741
Leu Phe Cys Val Phe Tyr Gly Leu Phe Gly Val Pro Leu Cys Leu Thr
        115                 120                 125
tgg atc agt gcc ctg ggc aag ttc ttc ggg gga cgt gcc aag aga cta      789
Trp Ile Ser Ala Leu Gly Lys Phe Phe Gly Gly Arg Ala Lys Arg Leu
    130                 135                 140
ggg cag ttc ctt acc aag aga ggt gtg agt ctg cgg aag gcg cag atc      837
Gly Gln Phe Leu Thr Lys Arg Gly Val Ser Leu Arg Lys Ala Gln Ile
145                 150                 155                 160
acg tgc aca gtc atc ttc atc gtg tgg ggc gtc cta gtc cac ctg gtg      885
Thr Cys Thr Val Ile Phe Ile Val Trp Gly Val Leu Val His Leu Val
                165                 170                 175
atc cca ccc ttc gta ttc atg gtg act gag ggg tgg aac tac atc gag      933
Ile Pro Pro Phe Val Phe Met Val Thr Glu Gly Trp Asn Tyr Ile Glu
            180                 185                 190
ggc ctc tac tac tcc ttc atc acc atc tcc acc atc ggc ttc ggt gac      981
Gly Leu Tyr Tyr Ser Phe Ile Thr Ile Ser Thr Ile Gly Phe Gly Asp
        195                 200                 205
ttt gtg gcc ggt gtg aac ccc agc gcc aac tac cac gcc ctg tac cgc     1029
Phe Val Ala Gly Val Asn Pro Ser Ala Asn Tyr His Ala Leu Tyr Arg
    210                 215                 220
tac ttc gtg gag ctc tgg atc tac ttg ggg ctg gcc tgg ctg tcc ctt     1077
Tyr Phe Val Glu Leu Trp Ile Tyr Leu Gly Leu Ala Trp Leu Ser Leu
225                 230                 235                 240
ttt gtc aac tgg aag gtg agc atg ttt gtg gaa gtc cac aaa gcc att     1125
Phe Val Asn Trp Lys Val Ser Met Phe Val Glu Val His Lys Ala Ile
                245                 250                 255
aag aag cgg cgg cgg cga cgg aag gag tcc ttt gag agc tcc cca cac     1173
Lys Lys Arg Arg Arg Arg Arg Lys Glu Ser Phe Glu Ser Ser Pro His
            260                 265                 270
```

```
tcc cgg aag gcc ctg cag gtg aag ggg agc aca gcc tcc aag gac gtc      1221
Ser Arg Lys Ala Leu Gln Val Lys Gly Ser Thr Ala Ser Lys Asp Val
        275                 280                 285
aac atc ttc agc ttt ctt tcc aag aag gaa gag acc tac aac gac ctc      1269
Asn Ile Phe Ser Phe Leu Ser Lys Lys Glu Glu Thr Tyr Asn Asp Leu
    290                 295                 300
atc aag cag atc ggg aag aag gcc atg aag aca agc ggg ggt ggg gag      1317
Ile Lys Gln Ile Gly Lys Lys Ala Met Lys Thr Ser Gly Gly Gly Glu
305                 310                 315                 320
acg ggc ccg ggc cca ggg ctg ggg cct caa ggc ggt ggg ctc cca gca      1365
Thr Gly Pro Gly Pro Gly Leu Gly Pro Gln Gly Gly Gly Leu Pro Ala
                325                 330                 335
ctg ccc cct tcc ctg gtg ccc ctg gta gtc tac tcc aag aac cgg gtg      1413
Leu Pro Pro Ser Leu Val Pro Leu Val Val Tyr Ser Lys Asn Arg Val
            340                 345                 350
ccc acc ttg gaa gag gtg tca cag aca ctg agg agc aaa ggc cac gta      1461
Pro Thr Leu Glu Glu Val Ser Gln Thr Leu Arg Ser Lys Gly His Val
        355                 360                 365
tca agg tcc cca gat gag gag gct gtg gca cgg gcc cct gaa gac agc      1509
Ser Arg Ser Pro Asp Glu Glu Ala Val Ala Arg Ala Pro Glu Asp Ser
    370                 375                 380
tcc cct gcc ccc gag gtg ttc atg aac cag ctg gac cgc atc agc gag      1557
Ser Pro Ala Pro Glu Val Phe Met Asn Gln Leu Asp Arg Ile Ser Glu
385                 390                 395                 400
gaa tgc gag cca tgg gac gcc cag gac tac cac cca ctc atc ttc cag      1605
Glu Cys Glu Pro Trp Asp Ala Gln Asp Tyr His Pro Leu Ile Phe Gln
                405                 410                 415
gac gcc agc atc acc ttc gtg aac acg gag gct ggc ctc tca gac gag      1653
Asp Ala Ser Ile Thr Phe Val Asn Thr Glu Ala Gly Leu Ser Asp Glu
            420                 425                 430
gag acc tcc aag tcc tcg cta gag gac aac ttg gca ggg gag gag agc      1701
Glu Thr Ser Lys Ser Ser Leu Glu Asp Asn Leu Ala Gly Glu Glu Ser
        435                 440                 445
ccc cag cag ggg gct gaa gcc aag gcg ccc ctg aac atg ggc gag ttc      1749
Pro Gln Gln Gly Ala Glu Ala Lys Ala Pro Leu Asn Met Gly Glu Phe
```



```
    450                 455                 460
ccc tcc tcc tcc gag tcc acc ttc acc agc act gag tct gag ctc tct      1797
Pro Ser Ser Ser Glu Ser Thr Phe Thr Ser Thr Glu Ser Glu Leu Ser
465                 470                 475                 480
gtg cct tac gaa cag ctg atg aat gag tac aac aag gct aac agc ccc      1845
Val Pro Tyr Glu Gln Leu Met Asn Glu Tyr Asn Lys Ala Asn Ser Pro
                485                 490                 495
aag ggc aca tgaggcaggg ccggctcccc accccacctt tgatgg                  1890
Lys Gly Thr

cctcttcccc cctcacccta gggtgtcccg agatgaccgg gacgcctggc ccctggtggg    1950
ggggcagcct cggaactggg agtgggggc caggggcctt cctaaccttc catcatcccc     2010
agctagatgt atgcccggga cagggcctct gttctccagc tgaaccatac cctggctgtg    2070
ggggcatctg tcctgagctt ggctggtgta tctcacaatg caaagacatg ctggctggcg    2130
ggacaggtgg gcaggactga ccctgaggag gccttgcctg cagggtcttt gtcccaccat    2190
ttggtggagt atcacacggt tctctgaggt ccggggcctc agctgtttaa gtttaccggt    2250
attactgagc tcggcatttg gagagggagc tctgaagtgt ctggggaggt accgctgtgc    2310
gtggggtcag gtgtttccgt accacagcag gagcagggcc cgcccgcatc ccagctgtgg    2370
gcctgccggt caggtcgggc acctactaca aaccgtagtg gggtggaggc tgctggaggt    2430
gggagtgagg agatgagggc agggtctcaa acagtcctga ctcacagggc ctggaaacaa    2490
gtcctatgtg ggcctggggc ctggggtcct catcctcctt gttggtctac tcaggcccag    2550
cccagagctg tgttccctgt ctcaggtcaa gcagtggcag acgcaaggct ttctgtgggc    2610
ccccaagtgg taggagggag agtagcagag catgggttac tggaagccgg gactgctagg    2670
gctggtggcc agggagctgc aagagtgagg ctcagctctg gctggttctg cccttacccc    2730
tcctgcccgc cggagaactg cacaccctgc ccgctggccc caggacctgc actcccaatc    2790
ctgctgtctt ctccttccct gtgccctgaa caaggacctc actgcccgcc ttcccctccc    2850
accagccccc ttgggccagg caggtgaggc ccaaattgct cttggcccac aaatgggtga    2910
tggtcagata tgtgaatcaa gctcctttct ctagctagtg tttgatgtgc acgtgtgtgt    2970
gcacagtgcg tgtgtgcaca cgcacacctg tgcactcgtg tgtgtttaag aaaggaaagg    3030
atttgggctg gggagcaaaa gataatgtga aactgttggt ggactctctg gtgaggggtg    3090
ggcagaactt gctgctacta gagttcttgg gttctccatg atgttcaccc tggggctggc    3150
ccactgtgtc ctgaatgttt ttgttatttt ttgttttatt ttttaaacaa actgctgttt    3210
ttatatacct ggaatctgtt gttggcttca gagccagtgg ttaaagagca gggtcccaag    3270
gattgggaga tctagtgtct gccctcctgc cctgcaactc aattgggcct ttttcggtga    3330
cctcatccaa ggccatgatg tcaagggcca tgtccccaag cagaggtgga gaaggggaca    3390
```

```
ctgaggtgag caaaagcagg aaggggcatc cactgcgggt gactggaggc cgggcaggaa   3450
gcaagtcatc agagccgctc agctccgttc actctctgcc ttctgcccca ctactgtggg   3510
gcagtggggc cagagcccac ctccccaaca tgtgaagaca gtgatgggca cgtgcccaca   3570
cccccacttc tctagccgtt tgcagaggcc gccacccagc aggggcctga aaaggagcag   3630
cctcgtattt ttctgtgaaa tgttttaatg aaccatgttg ttgctggttg tcctggcatc   3690
gcgcacactg tatgtacata ctggcaacga tgtcaaatgt aatttatttt aacattttta   3750
caataaaaca tgaggtgg                                                 3768
```

<210> 89
<211> 770
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (24)...(344)

<400> 89

```
accgcgaagg gaggagtggc aac atg gcg tct tcg gga gct ggt gac cct ctg    53
                          Met Ala Ser Ser Gly Ala Gly Asp Pro Leu
                           1               5                  10
gat tct aag cgt gga gag gcc ccg ttc gct cag cgt atc gac ccg act     101
Asp Ser Lys Arg Gly Glu Ala Pro Phe Ala Gln Arg Ile Asp Pro Thr
                15                  20                  25
cgg gag aag ctg aca ccc gag caa ctg cat tcc atg cgg cag gcg gag     149
Arg Glu Lys Leu Thr Pro Glu Gln Leu His Ser Met Arg Gln Ala Glu
            30                  35                  40
ctt gcc cag tgg cag aag gtc cta cca cgg cgg cga acc cgg aac atc     197
Leu Ala Gln Trp Gln Lys Val Leu Pro Arg Arg Arg Thr Arg Asn Ile
        45                  50                  55
gtg acc ggc cta ggc atc ggg gcc ctg gtg ttg gct att tat ggt tac     245
Val Thr Gly Leu Gly Ile Gly Ala Leu Val Leu Ala Ile Tyr Gly Tyr
    60                  65                  70
acc ttc tac tcg att tcc cag gag cgt ttc cta gat gag cta gaa gac     293
Thr Phe Tyr Ser Ile Ser Gln Glu Arg Phe Leu Asp Glu Leu Glu Asp
 75                  80                  85                  90
```



```
gag gcc aaa gct gcc cga gcc cga gct ctg gca agg gcg tca ggg tcc     341
Glu Ala Lys Ala Ala Arg Ala Arg Ala Leu Ala Arg Ala Ser Gly Ser
                95                 100                 105
taatctgga tgggtattga tcatgtccaa cctgctggag ccccttcaca tggtggatga    400
tgccccatga ccctgtagaa attgaatcct gctcacaaca ttgttggcct tcttactaac   460
cttggaccgt gattgagccc aagaaaccag ggacttacgc atttggccaa tgtcaaaaga   520
acagaacttt gcccactgca cacttgctgt gtacaatgac tgagcccttt cttgtagttt   580
gtttccttgt ttgagaggtg tgcatgcgac cgtggctttt cccaaagttt ctgactttgt   640
ggtttacccc cttcaccttc cagggacgca gttgttacga ggttagacgt ggcagctctg   700
tgcagtgttt gagcctacag tgggatacat agggtcaaat tgagaataat aaactgagtc   760
attctcctgg                                                          770
```

<210> 90
<211> 1229
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (96)...(554)

<400> 90

```
cctactcctg gattaggagg actgacaata ctacatatat cattaagcat gggcctcgct    60
tagaagttgc atctgagaaa gtagcccaga agaca atg gac tat gtg tgc tgt      113
                                       Met Asp Tyr Val Cys Cys
                                        1               5
gct tac aac aac ata acc ggc agg caa gat gaa act cat ttc aca gtt     161
Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu Thr His Phe Thr Val
            10                  15                  20
atc atc act tcc gta gga ctg gag aag ctt gca cag aaa gga aaa tca     209
Ile Ile Thr Ser Val Gly Leu Glu Lys Leu Ala Gln Lys Gly Lys Ser
        25                  30                  35
ttg tca cct tta gca agt ata act gga ata tca cta ttt ttg att ata     257
Leu Ser Pro Leu Ala Ser Ile Thr Gly Ile Ser Leu Phe Leu Ile Ile
    40                  45                  50
tcc atg tgt ctt ctc ttc cta tgg aaa aaa tat caa ccc tac aaa gtt     305
```

```
Ser Met Cys Leu Leu Phe Leu Trp Lys Lys Tyr Gln Pro Tyr Lys Val
 55                  60                  65                  70
ata aaa cag aaa cta gaa ggc agg cca gaa aca gaa tac agg aaa gct      353
Ile Lys Gln Lys Leu Glu Gly Arg Pro Glu Thr Glu Tyr Arg Lys Ala
                 75                  80                  85
caa aca ttt tca ggc cat gaa gat gct ctg gat gac ttc gga ata tat      401
Gln Thr Phe Ser Gly His Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr
             90                  95                 100
gaa ttt gtt gct ttt cca gat gtt tct ggt gtt tcc agg atc cca agc      449
Glu Phe Val Ala Phe Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser
        105                 110                 115
agg tct gtt cca gcc tct gat tgt gta tcg ggg caa gat ttg cac agt      497
Arg Ser Val Pro Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser
    120                 125                 130
aca gtg tat gaa gtt att cag cac atc cct gcc cag cag caa gac cat      545
Thr Val Tyr Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His
135                 140                 145                 150
cca gag tgaactttca tgggctaaac agtacattcg agtgaaattc tgaagaaac         600
Pro Glu

atttaagga aaaacagtgg aaaagtatat taatctggaa tcagtgaaga aaccaagacc     660
aacacctctt actcattatt cctttacatg cagaatagag gcatttatgc aaattgaact    720
gcaggttttt cagcatatac acaatgtctt gtgcaacaga aaaacatgtt ggggaaatat    780
tcctcagtgg agagtcgttc tcatgctgac ggggagaacg aaagtgacag gggtttcctc    840
ataagttttg tatgaaatat ctctacaaac ctcaattagt tctactctac actttcacta    900
tcatcaacac tgagactatc ctgtctcacc tacaaatgtg gaaactttac attgttcgat    960
ttttcagcag actttgtttt attaaatttt tattagtgtt aagaatgcta aagtttcaat   1020
tttatttcca aatttctatc ttgttatttg tacaacaaag taataaggat ggttgtcaca   1080
aaaacaaaac tatgccttct cttttttttc aatcaccagt agtattttg agaagacttg    1140
tgaacactta aggaaatgac tattaaagtc ttatttttat ttttttcaag gaaagatgga   1200
ttcaaataaa ttattctgtt tttgctttt                                     1229

<210> 91
<211> 358
<212> PRT
```



```
<213> Homo sapience

<400> 91
Met Ala Pro Gln Asn Leu Ser Thr Phe Cys Leu Leu Leu Leu Tyr Leu
  1               5                  10                  15
Ile Gly Ala Val Ile Ala Gly Arg Asp Phe Tyr Lys Ile Leu Gly Val
             20                  25                  30
Pro Arg Ser Ala Ser Ile Lys Asp Ile Lys Lys Ala Tyr Arg Lys Leu
         35                  40                  45
Ala Leu Gln Leu His Pro Asp Arg Asn Pro Asp Asp Pro Gln Ala Gln
     50                  55                  60
Glu Lys Phe Gln Asp Leu Gly Ala Ala Tyr Glu Val Leu Ser Asp Ser
 65                  70                  75                  80
Glu Lys Arg Lys Gln Tyr Asp Thr Tyr Gly Glu Glu Gly Leu Lys Asp
                 85                  90                  95
Gly His Gln Ser Ser His Gly Asp Ile Phe Ser His Phe Phe Gly Asp
            100                 105                 110
Phe Gly Phe Met Phe Gly Gly Thr Pro Arg Gln Gln Asp Arg Asn Ile
        115                 120                 125
Pro Arg Gly Ser Asp Ile Ile Val Asp Leu Glu Val Thr Leu Glu Glu
    130                 135                 140
Val Tyr Ala Gly Asn Phe Val Glu Val Val Arg Asn Lys Pro Val Ala
145                 150                 155                 160
Arg Gln Ala Pro Gly Lys Arg Lys Cys Asn Cys Arg Gln Glu Met Arg
                165                 170                 175
Thr Thr Gln Leu Gly Pro Gly Arg Phe Gln Met Thr Gln Glu Val Val
            180                 185                 190
Cys Asp Glu Cys Pro Asn Val Lys Leu Val Asn Glu Glu Arg Thr Leu
        195                 200                 205
Glu Val Glu Ile Glu Pro Gly Val Arg Asp Gly Met Glu Tyr Pro Phe
    210                 215                 220
Ile Gly Glu Gly Glu Pro His Val Asp Gly Glu Pro Gly Asp Leu Arg
225                 230                 235                 240
Phe Arg Ile Lys Val Val Lys His Pro Ile Phe Glu Arg Arg Gly Asp
                245                 250                 255
```

Asp Leu Tyr Thr Asn Val Thr Ile Ser Leu Val Glu Ser Leu Val Gly
260 265 270

Phe Glu Met Asp Ile Thr His Leu Asp Gly His Lys Val His Ile Ser
275 280 285

Arg Asp Lys Ile Thr Arg Pro Gly Ala Lys Leu Trp Lys Lys Gly Glu
290 295 300

Gly Leu Pro Asn Phe Asp Asn Asn Asn Ile Lys Gly Ser Leu Ile Ile
305 310 315 320

Thr Phe Asp Val Asp Phe Pro Lys Glu Gln Leu Thr Glu Glu Ala Arg
325 330 335

Glu Gly Ile Lys Gln Leu Leu Lys Gln Gly Ser Val Gln Lys Val Tyr
340 345 350

Asn Gly Leu Gln Gly Tyr
355

<210> 92
<211> 226
<212> PRT
<213> Homo sapience

<400> 92
Met Lys Met Val Ala Pro Trp Thr Arg Phe Tyr Ser Asn Ser Cys Cys
1 5 10 15

Leu Cys Cys His Val Arg Thr Gly Thr Ile Leu Leu Gly Val Trp Tyr
20 25 30

Leu Ile Ile Asn Ala Val Val Leu Leu Ile Leu Leu Ser Ala Leu Ala
35 40 45

Asp Pro Asp Gln Tyr Asn Phe Ser Ser Ser Glu Leu Gly Gly Asp Phe
50 55 60

Glu Phe Met Asp Asp Ala Asn Met Cys Ile Ala Ile Ala Ile Ser Leu
65 70 75 80

Leu Met Ile Leu Ile Cys Ala Met Ala Thr Tyr Gly Ala Tyr Lys Gln
85 90 95

Arg Ala Ala Trp Ile Ile Pro Phe Phe Cys Tyr Gln Ile Phe Asp Phe
100 105 110

Ala Leu Asn Met Leu Val Ala Ile Thr Val Leu Ile Tyr Pro Asn Ser
115 120 125

Ile Gln Glu Tyr Ile Arg Gln Leu Pro Pro Asn Phe Pro Tyr Arg Asp
130 135 140

Asp Val Met Ser Val Asn Pro Thr Cys Leu Val Leu Ile Ile Leu Leu
145 150 155 160

Phe Ile Ser Ile Ile Leu Thr Phe Lys Gly Tyr Leu Ile Ser Cys Val
165 170 175

Trp Asn Cys Tyr Arg Tyr Ile Asn Gly Arg Asn Ser Ser Asp Val Leu
180 185 190

Val Tyr Val Thr Ser Asn Asp Thr Thr Val Leu Leu Pro Pro Tyr Asp
195 200 205

Asp Ala Thr Val Asn Gly Ala Ala Lys Glu Pro Pro Pro Pro Tyr Val
210 215 220

Ser Ala
225

<210> 93
<211> 195
<212> PRT
<213> Homo sapience

<400> 93
Met Arg Leu Leu Leu Leu Leu Leu Val Ala Ala Ser Ala Met Val Arg
1 5 10 15

Ser Glu Ala Ser Ala Asn Leu Gly Gly Val Pro Ser Lys Arg Leu Lys
20 25 30

Met Gln Tyr Ala Thr Gly Pro Leu Leu Lys Phe Gln Ile Cys Val Ser
35 40 45

Xaa Gly Tyr Arg Arg Val Phe Glu Glu Tyr Met Arg Val Ile Ser Gln
50 55 60

Arg Tyr Pro Asp Ile Arg Ile Glu Gly Glu Asn Tyr Leu Pro Gln Pro
65 70 75 80

Ile Tyr Arg His Ile Ala Ser Phe Leu Ser Val Phe Lys Leu Val Leu
85 90 95

```
Ile Gly Leu Ile Ile Val Gly Lys Asp Pro Phe Ala Phe Phe Gly Met
            100                 105                 110
Gln Ala Pro Ser Ile Trp Gln Trp Gly Gln Glu Asn Lys Val Tyr Ala
        115                 120                 125
Cys Met Met Val Phe Phe Leu Ser Asn Met Ile Glu Asn Gln Cys Met
    130                 135                 140
Ser Thr Gly Ala Phe Glu Ile Thr Leu Asn Asp Val Pro Val Trp Ser
145                 150                 155                 160
Lys Leu Glu Ser Gly His Leu Pro Ser Met Gln Gln Leu Val Gln Ile
                165                 170                 175
Leu Asp Asn Glu Met Lys Leu Asn Val His Met Asp Ser Ile Pro His
            180                 185                 190
His Arg Ser
        195
```

<210> 94
<211> 339
<212> PRT
<213> Homo sapience

<400> 94

```
Met Asn Trp Glu Leu Leu Leu Trp Leu Leu Val Leu Cys Ala Leu Leu
 1               5                  10                  15
Leu Leu Leu Val Gln Leu Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu
            20                  25                  30
Thr Leu Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu
        35                  40                  45
Thr Asp Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu
    50                  55                  60
Glu Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser
65                  70                  75                  80
Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu Glu
                85                  90                  95
Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu Asp Leu
            100                 105                 110
```



```
Thr Asp Thr Gly Ser His Glu Ala Ala Thr Lys Ala Val Leu Gln Glu
        115                 120                 125
Phe Gly Arg Ile Asp Ile Leu Val Asn Asn Gly Gly Met Ser Gln Arg
    130                 135                 140
Ser Leu Cys Met Asp Thr Ser Leu Asp Val Tyr Arg Lys Leu Ile Glu
145                 150                 155                 160
Leu Asn Tyr Leu Gly Thr Val Ser Leu Thr Lys Cys Val Leu Pro His
                165                 170                 175
Met Ile Glu Arg Lys Gln Gly Lys Ile Val Thr Val Asn Ser Ile Leu
            180                 185                 190
Gly Ile Ile Ser Val Pro Leu Ser Ile Gly Tyr Cys Ala Ser Lys His
        195                 200                 205
Ala Leu Arg Gly Phe Phe Asn Gly Leu Arg Thr Glu Leu Ala Thr Tyr
    210                 215                 220
Pro Gly Ile Ile Val Ser Asn Ile Cys Pro Gly Pro Val Gln Ser Asn
225                 230                 235                 240
Ile Val Glu Asn Ser Leu Ala Gly Glu Val Thr Lys Thr Ile Gly Asn
                245                 250                 255
Asn Gly Asp Gln Ser His Lys Met Thr Thr Ser Arg Cys Val Arg Leu
            260                 265                 270
Met Leu Ile Ser Met Ala Asn Asp Leu Lys Glu Val Trp Ile Ser Glu
        275                 280                 285
Gln Pro Phe Leu Leu Val Thr Tyr Leu Trp Gln Tyr Met Pro Thr Trp
    290                 295                 300
Ala Trp Trp Ile Thr Asn Lys Met Gly Lys Lys Arg Ile Glu Asn Phe
305                 310                 315                 320
Lys Ser Gly Val Asp Ala Asp Ser Ser Tyr Phe Lys Ile Phe Lys Thr
                325                 330                 335
Lys His Asp
```

<210> 95
<211> 487
<212> PRT
<213> Homo sapience

```
<400> 95
Met Asp Gly Thr Glu Thr Arg Gln Arg Arg Leu Asp Ser Cys Gly Lys
1               5                   10                  15
Pro Gly Glu Leu Gly Leu Pro His Pro Leu Ser Thr Gly Gly Leu Pro
            20                  25                  30
Val Ala Ser Glu Asp Gly Ala Leu Arg Ala Pro Glu Ser Gln Ser Val
        35                  40                  45
Thr Pro Lys Pro Leu Glu Thr Glu Pro Ser Arg Glu Thr Ala Trp Ser
    50                  55                  60
Ile Gly Leu Gln Val Thr Val Pro Phe Met Phe Ala Gly Leu Gly Leu
65                  70                  75                  80
Ser Trp Ala Gly Met Leu Leu Asp Tyr Phe Gln His Trp Pro Val Phe
                85                  90                  95
Val Glu Val Lys Asp Leu Leu Thr Leu Val Pro Pro Leu Val Gly Leu
            100                 105                 110
Lys Gly Asn Leu Glu Met Thr Leu Ala Ser Arg Leu Ser Thr Ala Ala
        115                 120                 125
Asn Thr Gly Gln Ile Asp Asp Pro Gln Glu Gln His Arg Val Ile Ser
    130                 135                 140
Ser Asn Leu Ala Leu Ile Gln Val Gln Ala Thr Val Val Gly Leu Leu
145                 150                 155                 160
Ala Ala Val Ala Ala Leu Leu Leu Gly Val Val Ser Arg Glu Glu Val
                165                 170                 175
Asp Val Ala Lys Val Glu Leu Leu Cys Ala Ser Ser Val Leu Thr Ala
            180                 185                 190
Phe Leu Ala Ala Phe Ala Leu Gly Val Leu Met Val Cys Ile Val Ile
        195                 200                 205
Gly Ala Arg Lys Leu Gly Val Asn Pro Asp Asn Ile Ala Thr Pro Ile
    210                 215                 220
Ala Ala Ser Leu Gly Asp Leu Ile Thr Leu Ser Ile Leu Ala Leu Val
225                 230                 235                 240
Ser Ser Phe Phe Tyr Arg His Lys Asp Ser Arg Tyr Leu Thr Pro Leu
                245                 250                 255
Val Cys Leu Ser Phe Ala Ala Leu Thr Pro Val Trp Val Leu Ile Ala
            260                 265                 270
```



```
Lys Gln Ser Pro Pro Ile Val Lys Ile Leu Lys Phe Gly Trp Phe Pro
        275                 280                 285
Ile Ile Leu Ala Met Val Ile Ser Ser Phe Gly Gly Leu Ile Leu Ser
    290                 295                 300
Lys Thr Val Ser Lys Gln Gln Tyr Lys Gly Met Ala Ile Phe Thr Pro
305                 310                 315                 320
Val Ile Cys Gly Val Gly Gly Asn Leu Val Ala Ile Gln Thr Ser Arg
                325                 330                 335
Ile Ser Thr Tyr Leu His Met Trp Ser Ala Pro Gly Val Leu Pro Leu
            340                 345                 350
Gln Met Lys Lys Phe Trp Pro Asn Pro Cys Ser Thr Phe Cys Thr Ser
        355                 360                 365
Glu Ile Asn Ser Met Ser Ala Arg Val Leu Leu Leu Val Val Pro
    370                 375                 380
Gly His Leu Ile Phe Phe Tyr Ile Ile Tyr Leu Val Glu Gly Gln Ser
385                 390                 395                 400
Val Ile Asn Ser Gln Thr Phe Val Val Leu Tyr Leu Leu Ala Gly Leu
                405                 410                 415
Ile Gln Val Thr Ile Leu Leu Tyr Leu Ala Glu Val Met Val Arg Leu
            420                 425                 430
Thr Trp His Gln Ala Leu Asp Pro Asp Asn His Cys Ile Pro Tyr Leu
        435                 440                 445
Thr Gly Leu Gly Asp Leu Leu Gly Thr Gly Leu Leu Ala Leu Cys Phe
    450                 455                 460
Phe Thr Asp Trp Leu Leu Lys Ser Lys Ala Glu Leu Gly Gly Ile Ser
465                 470                 475                 480
Glu Leu Ala Ser Gly Pro Pro
                485

<210> 96
<211> 393
<212> PRT
<213> Homo sapience

<400> 96
```

Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
1 5 10 15
Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys
20 25 30
Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg
35 40 45
Gly Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val Val Leu Glu His
50 55 60
Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His Phe Ala Gly Asp
65 70 75 80
Val Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr Asp Val Thr
85 90 95
Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp Leu Gln
100 105 110
Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu His Asp
115 120 125
Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys Gly Leu
130 135 140
His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp Asp Phe
145 150 155 160
Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser Lys Thr
165 170 175
Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val Val Glu
180 185 190
Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile His Met
195 200 205
Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu Ala Leu
210 215 220
Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu Gly Met
225 230 235 240
Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp Gly Phe
245 250 255
Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly Pro Asn
260 265 270
Ala Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp Pro Lys

275 280 285
Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe Tyr Gly Met
290 295 300
Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu Pro Val Val Gly Ala Arg
305 310 315 320
Tyr Ile Gln Thr Leu Lys Asp His Arg Pro Arg Met Val Trp Asp Ser
325 330 335
Gln Ala Ser Glu His Phe Phe Glu Tyr Lys Lys Ser Arg Ser Gly Arg
340 345 350
His Val Val Phe Tyr Pro Thr Leu Lys Ser Leu Gln Val Arg Leu Glu
355 360 365
Leu Ala Arg Glu Leu Gly Val Gly Val Ser Ile Trp Glu Leu Gly Gln
370 375 380
Gly Leu Asp Tyr Phe Tyr Asp Leu Leu
385 390

<210> 97
<211> 196
<212> PRT
<213> Homo sapience

<400> 97
Met Trp Arg Val Pro Gly Thr Thr Arg Arg Pro Val Thr Gly Glu Ser
1 5 10 15
Pro Gly Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala
20 25 30
Leu Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly
35 40 45
Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr Gly
50 55 60
Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln Val Lys
65 70 75 80
Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly Gly Asn Thr
85 90 95
Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr Lys Val Phe Val

```
        100                 105                 110
Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met Tyr Thr Ser Lys Asp
    115                 120                 125
Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly Gln Ile Ser Ser Ala Tyr
    130                 135                 140
Pro Ser Gln Glu Gly Gln Val Leu Val Gly Ile Tyr Gly Gln Tyr Gln
145                 150                 155                 160
Leu Leu Gly Ile Lys Ser Ile Gly Phe Glu Trp Asn Tyr Pro Leu Glu
                165                 170                 175
Glu Pro Thr Thr Glu Pro Pro Val Asn Leu Thr Tyr Ser Ala Asn Ser
            180                 185                 190
Pro Val Gly Arg
        195

&lt;210&gt; 98
&lt;211&gt; 107
&lt;212&gt; PRT
&lt;213&gt; Homo sapience

&lt;400&gt; 98
Met Glu Gln Lys Leu Val Glu Glu Ile Leu Gln Ala Ile Thr Met Ser
  1               5                  10                  15
Thr Asp Thr Gly Val Ser Leu Pro Ser Tyr Glu Glu Asp Gln Gly Ser
            20                  25                  30
Lys Leu Ile Arg Lys Ala Lys Glu Ala Pro Phe Val Pro Val Gly Ile
        35                  40                  45
Ala Gly Phe Ala Ala Ile Val Ala Tyr Gly Leu Tyr Lys Leu Lys Ser
    50                  55                  60
Arg Gly Asn Thr Lys Met Ser Ile His Leu Ile His Met Arg Val Ala
65                  70                  75                  80
Ala Glu Gly Phe Val Val Gly Ala Met Thr Val Gly Met Gly Tyr Ser
                85                  90                  95
Met Tyr Arg Glu Phe Trp Ala Lys Pro Lys Pro
            100                 105
```



```
&lt;210&gt; 99
&lt;211&gt; 350
&lt;212&gt; PRT
&lt;213&gt; Homo sapience

&lt;400&gt; 99
Met Ser Glu Val Lys Ser Arg Lys Lys Ser Gly Pro Lys Gly Ala Pro
  1               5                  10                  15
Ala Ala Glu Pro Gly Lys Arg Ser Glu Gly Gly Lys Thr Pro Val Ala
            20                  25                  30
Arg Ser Ser Gly Gly Gly Gly Trp Ala Asp Pro Arg Thr Cys Leu Ser
        35                  40                  45
Leu Leu Ser Leu Gly Thr Cys Leu Gly Leu Ala Trp Phe Val Phe Gln
    50                  55                  60
Gln Ser Glu Lys Phe Ala Lys Val Glu Asn Gln Tyr Gln Leu Leu Lys
65                  70                  75                  80
Leu Glu Thr Asn Glu Phe Gln Gln Leu Gln Ser Lys Ile Ser Leu Ile
                85                  90                  95
Ser Glu Lys Trp Gln Lys Ser Glu Ala Ile Met Glu Gln Leu Lys Ser
            100                 105                 110
Phe Gln Ile Ile Ala His Leu Lys Arg Leu Gln Glu Glu Ile Asn Glu
        115                 120                 125
Val Lys Thr Trp Ser Asn Arg Ile Thr Glu Lys Gln Asp Ile Leu Asn
    130                 135                 140
Asn Ser Leu Thr Thr Leu Ser Gln Asp Ile Thr Lys Val Asp Gln Ser
145                 150                 155                 160
Thr Thr Ser Met Ala Lys Asp Val Gly Leu Lys Ile Thr Ser Val Lys
                165                 170                 175
Thr Asp Ile Arg Arg Ile Ser Gly Leu Val Thr Asp Val Ile Ser Leu
            180                 185                 190
Thr Asp Ser Val Gln Glu Leu Glu Asn Lys Ile Glu Lys Val Glu Lys
        195                 200                 205
Asn Thr Val Lys Asn Ile Gly Asp Leu Leu Ser Ser Ser Ile Asp Arg
    210                 215                 220
Thr Ala Thr Leu Arg Lys Thr Ala Ser Glu Asn Ser Gln Arg Ile Asn
```

```
225                 230                 235                 240
Ser Val Lys Lys Thr Leu Thr Glu Leu Lys Ser Asp Phe Asp Lys His
                245                 250                 255
Thr Asp Arg Phe Leu Ser Leu Glu Gly Asp Arg Ala Lys Val Leu Lys
            260                 265                 270
Thr Val Thr Phe Ala Asn Asp Leu Lys Pro Lys Val Tyr Asn Leu Lys
        275                 280                 285
Lys Asp Phe Ser Arg Leu Glu Pro Leu Val Asn Asp Leu Thr Leu Arg
    290                 295                 300
Ile Gly Arg Leu Val Thr Asp Leu Leu Gln Arg Glu Lys Glu Ile Ala
305                 310                 315                 320
Phe Leu Ser Glu Lys Ile Ser Asn Leu Thr Ile Val Gln Ala Glu Ile
                325                 330                 335
Lys Asp Ile Lys Asp Glu Ile Ala His Ile Ser Asp Met Asn
            340                 345                 350
```

<210> 100
<211> 107
<212> PRT
<213> Homo sapience

<400> 100

```
Met Ser Ser Ala Gly Thr Ala Thr Pro Leu Glu Met Asp His Lys Leu
  1               5                  10                  15
Thr Ser Gln Pro Gly Arg Pro Ser Phe Tyr Cys Asn Ser Arg His Ser
             20                  25                  30
Ile Val Gly Ser Ser His Gln Leu Gly Phe Trp Phe Ser His Leu Glu
         35                  40                  45
Ser Ser Gly Leu Lys Val Phe Gln Val Ser Leu Pro Cys Glu Cys Val
     50                  55                  60
Asn Leu Pro Thr Arg Ile Ala Ser Val Val Leu Ser Leu Met Ser Leu
 65                  70                  75                  80
Leu Val Val Gly Gln Ala Pro Ala Trp Glu Gly Ser Leu Leu Arg Gly
                 85                  90                  95
Arg Pro Ala Gly Gly Ala His Leu Cys Ala Ala
```



```
                100                 105
```

<210> 101
<211> 1074
<212> DNA
<213> Homo Sapience

<400> 101

```
atggctccgc agaacctgag cacctttgc ctgttgctgc tatacctcat cggggcggtg      60
attgccggac gagatttcta taagatcttg gggtgcctc gaagtgcctc tataaaggat     120
attaaaaagg cctataggaa actagccctg cagcttcatc ccgaccggaa ccctgatgat     180
ccacaagccc aggagaaatt ccaggatctg ggtgctgctt atgaggttct gtcagatagt     240
gagaaacgga aacagtacga tacttatggt gaagaaggat taaaagatgg tcatcagagc     300
tcccatggag acatttttc acacttcttt ggggattttg gtttcatgtt tggaggaacc     360
cctcgtcagc aagacagaaa tattccaaga ggaagtgata ttattgtaga tctagaagtc     420
actttggaag aagtatatgc aggaaatttt gtggaagtag ttagaaacaa acctgtggca     480
aggcaggctc ctggcaaacg gaagtgcaat tgtcggcaag agatgcggac cacccagctg     540
ggccctgggc gcttccaaat gacccaggag gtggtctgcg acgaatgccc taatgtcaaa     600
ctagtgaatg aagaacgaac gctggaagta gaaatagagc ctggggtgag agacggcatg     660
gagtacccct ttattggaga aggtgagcct cacgtggatg gggagcctgg agatttacgg     720
ttccgaatca aagttgtcaa gcacccaata tttgaaagga gaggagatga tttgtacaca     780
aatgtgacaa tctcattagt tgagtcactg gttggctttg agatggatat tactcacttg     840
gatggtcaca aggtacatat ttcccgggat aagatcacca ggccaggagc gaagctatgg     900
aagaaagggg aagggctccc caactttgac aacaacaata tcaagggctc tttgataatc     960
acttttgatg tggattttcc aaaagaacag ttaacagagg aagcgagaga aggtatcaaa    1020
cagctactga aacaagggtc agtgcagaag gtatacaatg gactgcaagg atat          1074
```

<210> 102
<211> 678
<212> DNA
<213> Homo Sapience

<400> 102

```
atgaagatgg tcgcgccctg gacgcggttc tactccaaca gctgctgctt gtgctgccat      60
gtccgcaccg gcaccatcct gctcggcgtc tggtatctga tcatcaatgc tgtggtactg     120
```

```
ttgattttat tgagtgccct ggctgatccg gatcagtata acttttcaag ttctgaactg     180
ggaggtgact ttgagttcat ggatgatgcc aacatgtgca ttgccattgc gatttctctt     240
ctcatgatcc tgatatgtgc tatggctact tacggagcgt acaagcaacg cgcagcctgg     300
atcatcccat tcttctgtta ccagatcttt gactttgccc tgaacatgtt ggttgcaatc     360
actgtgctta tttatccaaa ctccattcag gaatacatac ggcaactgcc tcctaatttt     420
ccctacagag atgatgtcat gtcagtgaat cctacctgtt tggtccttat tattcttctg     480
tttattagca ttatcttgac ttttaagggt tacttgatta gctgtgtttg gaactgctac     540
cgatacatca atggtaggaa ctcctctgat gtcctggttt atgttaccag caatgacact     600
acggtgctgc taccccccgta tgatgatgcc actgtgaatg gtgctgccaa ggagccaccg     660
ccaccttacg tgtctgcc                                                   678
```

<210> 103
<211> 585
<212> DNA
<213> Homo Sapience

<400> 103

```
atgaggcttc tgctgcttct cctagtggcg gcgtctgcga tggtccggag cgaggcctcg      60
gccaatctgg gcggcgtgcc cagcaagaga ttaaagatgc agtacgccac ggggccgctg     120
ctcaagttcc agatttgtgt ttcctgaggt tataggcggg tgtttgagga gtacatgcgg     180
gttattagcc agcggtaccc agacatccgc attgaaggag agaattacct ccctcaacca     240
atatatagac acatagcatc tttcctgtca gtcttcaaac tagtattaat aggcttaata     300
attgttggca aggatccttt tgctttcttt ggcatgcaag ctcctagcat ctggcagtgg     360
ggccaagaaa ataaggttta tgcatgtatg atggttttct tcttgagcaa catgattgag     420
aaccagtgta tgtcaacagg tgcatttgag ataactttaa atgatgtacc tgtgtggtct     480
aagctggaat ctggtcacct tccatccatg caacaacttg ttcaaattct tgacaatgaa     540
atgaagctca atgtgcatat ggattcaatc ccacaccatc gatca                     585
```

<210> 104
<211> 1017
<212> DNA
<213> Homo Sapience

<400> 104

```
atgaactggg agctgctgct gtggctgctg gtgctgtgcg cgctgctcct gctcttggtg      60
```



```
cagctgctgc gcttcctgag ggctgacggc gacctgacgc tactatgggc cgagtggcag     120
ggacgacgcc cagaatggga gctgactgat atggtggtgt gggtgactgg agcctcgagt     180
ggaattggtg aggagctggc ttaccagttg tctaaactag gagtttctct tgtgctgtca     240
gccagaagag tgcatgagct ggaaagggtg aaaagaagat gcctagagaa tggcaattta     300
aaagaaaaag atatacttgt tttgcccctt gacctgaccg acactggttc ccatgaagcg     360
gctaccaaag ctgttctcca ggagtttggt agaatcgaca ttctggtcaa caatggtgga     420
atgtcccagc gttctctgtg catggatacc agcttggatg tctacagaaa gctaatagag     480
cttaactact tagggacggt gtccttgaca aaatgtgttc tgcctcacat gatcgagagg     540
aagcaaggaa agattgttac tgtgaatagc atcctgggta tcatatctgt acctctttcc     600
attggatact gtgctagcaa gcatgctctc cggggttttt ttaatggcct tcgaacagaa     660
cttgccacat acccaggtat aatagtttct aacatttgcc caggacctgt gcaatcaaat     720
attgtggaga attccctagc tggagaagtc acaaagacta taggcaataa tggagaccag     780
tcccacaaga tgacaaccag tcgttgtgtg cggctgatgt taatcagcat ggccaatgat     840
ttgaaagaag tttggatctc agaacaacct ttcttgttag taacatattt gtggcaatac     900
atgccaacct gggcctggtg gataaccaac aagatgggga agaaaaggat tgagaacttt     960
aagagtggtg tggatgcaga ctcttcttat tttaaaatct ttaagacaaa acatgac       1017
```

<210> 105
<211> 1461
<212> DNA
<213> Homo Sapience

<400> 105

```
atggatggga cagagacccg gcagcggagg ctggacagct gtggcaagcc aggggagctg      60
gggcttcctc accccctcag cacaggagga ctccctgtag cctcagaaga tggagctctc     120
agggccccctg agagccaaag cgtgaccccc aagccactgg agactgagcc tagcagggag     180
accgcctggt ccataggcct tcaggtgacc gtgcccttca tgtttgcagg cctgggactg     240
tcctgggccg gcatgcttct ggactatttc cagcactggc ctgtgtttgt ggaggtgaaa     300
gacctttga cattggtgcc gcccctggtg ggcctgaagg ggaacctgga gatgacactg      360
gcatccagac tctccacagc tgccaacact ggacaaattg atgaccccca ggagcagcac     420
agagtcatca gcagcaacct ggccctcatc caggtgcagg ccactgtcgt ggggctcttg     480
gctgctgtgg ctgcgctgct gttgggcgtg gtgtctcgag aggaagtgga tgtcgccaag     540
gtggagttgc tgtgtgccag cagtgtcctc actgccttcc ttgcagcctt tgccctgggg     600
gtgctgatgg tctgtatagt gattggtgct cgaaagctcg ggtcaaccc agacaacatt      660
gccacgccca ttgcagccag cctgggagac ctcatcacac tgtccattct ggctttggtt     720
```

agcagcttct tctacagaca caaagatagt cggtatctga cgccgctggt ctgcctcagc 780
tttgcggctc tgaccccagt gtgggtcctc attgccaagc agagcccacc catcgtgaag 840
atcctgaagt ttggctggtt cccaatcatc ctggccatgg tcatcagcag tttcggagga 900
ctcatcttga gcaaaaccgt ttctaaacag cagtacaaag gcatggcgat atttaccccc 960
gtcatatgtg gtgttggtgg caatctggtg gccattcaga ccagccgaat ctcaacctac 1020
ctgcacatgt ggagtgcacc tggcgtcctg cccctccaga tgaagaaatt ctggcccaac 1080
ccgtgttcta ctttctgcac gtcagaaatc aattccatgt cagctcgagt cctgctcttg 1140
ctggtggtcc caggccatct gattttcttc tacatcatct acctggtgga gggtcagtca 1200
gtcataaaca gccagacctt tgtggtgctc tacctgctgg caggcctgat ccaggtgaca 1260
atcctgctgt acctggcaga agtgatggtt cggctgactt ggcaccaggc cctggatcct 1320
gacaaccact gcatccccta ccttacaggg ctgggggacc tgctcggtac tggcctcctg 1380
gcactctgct ttttcactga ctggctactg aagagcaagg cagagctggg tggcatctca 1440
gaactggcat ctggacctcc c 1461

<210> 106
<211> 1179
<212> DNA
<213> Homo Sapience

<400> 106
atgcggacac tcttcaacct cctctggctt gccctggcct gcagccctgt tcacactacc 60
ctgtcaaagt cagatgccaa aaaagccgcc tcaaagacgc tgctggagaa gagtcagttt 120
tcagataagc cggtgcaaga ccggggtttg gtggtgacgg acctcaaagc tgagagtgtg 180
gttcttgagc atcgcagcta ctgctcggca aaggcccggg acagacactt tgctggggat 240
gtactgggct atgtcactcc atggaacagc catggctacg atgtcaccaa ggtctttggg 300
agcaagttca cacagatctc acccgtctgg ctgcagctga agagacgtgg ccgtgagatg 360
tttgaggtca cgggcctcca cgacgtggac caagggtgga tgcgagctgt caggaagcat 420
gccaagggcc tgcacatagt gcctcggctc ctgtttgagg actggactta cgatgatttc 480
cggaacgtct tagacagtga ggatgagata gaggagctga gcaagaccgt ggtccaggtg 540
gcaaagaacc agcatttcga tggcttcgtg gtggaggtct ggaaccagct gctaagccag 600
aagcgcgtgg gcctcatcca catgctcacc cacttggccg aggctctgca ccaggcccgg 660
ctgctggccc tcctggtcat cccgcctgcc atcacccccg ggaccgacca gctgggcatg 720
ttcacgcaca aggagtttga gcagctggcc cccgtgctgg atggtttcag cctcatgacc 780
tacgactact ctacagcgca tcagcctggc cctaatgcac ccctgtcctg ggttcgagcc 840
tgcgtccagg tcctggaccc gaagtccaag tggcgaagca aaatcctcct ggggctcaac 900

ttctatggta tggactacgc gacctccaag gatgcccgtg agcctgttgt cggggccagg 960
tacatccaga cactgaagga ccacaggccc cggatggtgt gggacagcca ggcctcagag 1020
cacttcttcg agtacaagaa gagccgcagt gggaggcacg tcgtcttcta cccaaccctg 1080
aagtccctgc aggtgcggct ggagctggcc cgggagctgg gcgttggggt ctctatctgg 1140
gagctgggcc agggcctgga ctacttctac gacctgctc 1179

<210> 107
<211> 588
<212> DNA
<213> Homo Sapience

<400> 107
atgtggaggg tgcccggcac aaccagacgc ccagtcacag gcgagagccc tgggatgcac 60
cggccagagg ccatgctgct gctgctcacg cttgccctcc tgggggcccc cacctgggca 120
gggaagatgt atggccctgg aggaggcaag tatttcagca ccactgaaga ctacgaccat 180
gaaatcacag ggctgcgggt gtctgtaggt cttctcctgg tgaaaagtgt ccaggtgaaa 240
cttggagact cctgggacgt gaaactggga gccttaggtg ggaataccca ggaagtcacc 300
ctgcagccag gcgaatacat cacaaaagtc tttgtcgcct tccaagcttt cctccggggt 360
atggtcatgt acaccagcaa ggaccgctat ttctattttg ggaagcttga tggccagatc 420
tcctctgcct accccagcca agaggggcag gtgctggtgg gcatctatgg ccagtatcaa 480
ctccttggca tcaagagcat tggctttgaa tggaattatc cactagagga gccgaccact 540
gagccaccag ttaatctcac atactcagca aactcacccg tgggtcgc 588

<210> 108
<211> 321
<212> DNA
<213> Homo Sapience

<400> 108
atggagcaga agcttgtgga ggagattctt caagcaatca ctatgtcaac agacacaggt 60
gtttcccttc cttcatatga ggaagatcag ggatcaaaac tcattcgaaa agctaaagag 120
gcaccattcg tacccgttgg aatagcgggt tttgcagcaa ttgttgcata tggattatat 180
aaactgaaga gcaggggaaa tactaaaatg tccattcatc tgatccacat gcgtgtggca 240
gcccaaggct ttgttgtagg agcaatgact gttggtatgg gctattccat gtatcgggaa 300
ttctgggcaa aacctaagcc t 321

<210> 109
<211> 1050
<212> DNA
<213> Homo Sapience

<400> 109
```
atgtctgagg tgaagagccg gaagaagtcg gggcccaagg gagcccctgc tgcggagccc     60
gggaagcgga gcgagggcgg gaagaccccc gtggcccgga gcagcggagg cgggggctgg    120
gcagaccccc gaacgtgcct gagcctgctg tcgctgggga cgtgcctggg cctggcctgg    180
tttgtatttc agcagtcaga aaaatttgca aaggtggaaa accaatacca gttactgaaa    240
ctagaaacca atgaattcca acaacttcaa agtaaaatca gtttaatttc agaaaagtgg    300
cagaaatctg aagctatcat ggaacaattg aagtcttttc aaataattgc tcatctaaag    360
cgtctacagg aagaaattaa tgaggtaaaa acttggtcca ataggataac tgaaaaacag    420
gatatactga acaacagtct gacgacgctt tctcaagaca ttacaaaagt agaccaaagt    480
acaacttcca tggcaaaaga tgttggtctc aagattacaa gtgtaaaaac agatatacga    540
cggatttcag gtttagtaac tgatgtaata tcattgacag attctgtgca agaactagaa    600
aataaaatag agaaagtaga aaaaaataca gtaaaaaata taggtgatct tctttcaagc    660
agtattgatc gaacagcaac gctccgaaag acagcatctg aaaattcaca aagaattaac    720
tctgttaaga agacgctaac cgaactaaag agtgacttcg acaaacatac agatagattt    780
ctaagcttag aaggtgacag agccaaagtt ctgaagacag tgacttttgc aaatgatcta    840
aaaccaaagg tgtataatct aaagaaggac ttttcccgtt tagaaccatt agtaaatgat    900
ttaacactac gcattgggag attggttacc gacttactac aaagagagaa agaaattgct    960
ttcttaagtg aaaaaatatc taatttaaca atagtccaag ctgagattaa ggatattaaa   1020
gatgaaatag cacacatttc agatatgaat                                    1050
```

<210> 110
<211> 321
<212> DNA
<213> Homo Sapience

<400> 110
```
atgtcctcag caggcacagc aacccctctg gaaatggatc acaaactcac ttctcagcca     60
ggcaggccaa gcttctattg taacagtagg cacagtatag tcggatcatc acatcagctg    120
ggtttttggt ttagtcatct agagtcgtct ggactaaagg tctttcaggt ctccttgccc    180
```



```
tgtgagtgcg tgaacctccc caccсgaatt gcctcagttg tcctgagcct catgtctctc    240
ctggtggtgg gccaggcccc tgcatgggaa gggagcctgc tgcggggcag gccagctggg    300
ggtgctcacc tatgcgcagc a                                              321
```

<210> 111
<211> 1619
<212> DNA
<213> Homo Sapience
<220>
<221> CDS
<222> (158)...(1234)

<400> 111
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agaagagggg gctagctagc tgtctctgcg gaccagggag acccccgcgc ccccccggtg     60
tgaggcggcc tcacagggcc gggtgggctg gcgagccgac gcggcggcgg aggaggctgt    120
gaggagtgtg tggaacagga cccgggacag aggaacc atg gct ccg cag aac ctg    175
                                         Met Ala Pro Gln Asn Leu
                                           1               5
agc acc ttt tgc ctg ttg ctg cta tac ctc atc ggg gcg gtg att gcc      223
Ser Thr Phe Cys Leu Leu Leu Leu Tyr Leu Ile Gly Ala Val Ile Ala
            10                  15                  20
gga cga gat ttc tat aag atc ttg ggg gtg cct cga agt gcc tct ata      271
Gly Arg Asp Phe Tyr Lys Ile Leu Gly Val Pro Arg Ser Ala Ser Ile
        25                  30                  35
aag gat att aaa aag gcc tat agg aaa cta gcc ctg cag ctt cat ccc      319
Lys Asp Ile Lys Lys Ala Tyr Arg Lys Leu Ala Leu Gln Leu His Pro
    40                  45                  50
gac cgg aac cct gat gat cca caa gcc cag gag aaa ttc cag gat ctg      367
Asp Arg Asn Pro Asp Asp Pro Gln Ala Gln Glu Lys Phe Gln Asp Leu
55                  60                  65                  70
ggt gct gct tat gag gtt ctg tca gat agt gag aaa cgg aaa cag tac      415
Gly Ala Ala Tyr Glu Val Leu Ser Asp Ser Glu Lys Arg Lys Gln Tyr
                75                  80                  85
gat act tat ggt gaa gaa gga tta aaa gat ggt cat cag agc tcc cat      463
Asp Thr Tyr Gly Glu Glu Gly Leu Lys Asp Gly His Gln Ser Ser His
```

```
                90                       95                      100
gga gac att ttt tca cac ttc ttt ggg gat ttt ggt ttc atg ttt gga     511
Gly Asp Ile Phe Ser His Phe Phe Gly Asp Phe Gly Phe Met Phe Gly
        105                 110                 115
gga acc cct cgt cag caa gac aga aat att cca aga gga agt gat att     559
Gly Thr Pro Arg Gln Gln Asp Arg Asn Ile Pro Arg Gly Ser Asp Ile
    120                 125                 130
att gta gat cta gaa gtc act ttg gaa gaa gta tat gca gga aat ttt     607
Ile Val Asp Leu Glu Val Thr Leu Glu Glu Val Tyr Ala Gly Asn Phe
135                 140                 145                 150
gtg gaa gta gtt aga aac aaa cct gtg gca agg cag gct cct ggc aaa     655
Val Glu Val Val Arg Asn Lys Pro Val Ala Arg Gln Ala Pro Gly Lys
                155                 160                 165
cgg aag tgc aat tgt cgg caa gag atg cgg acc acc cag ctg ggc cct     703
Arg Lys Cys Asn Cys Arg Gln Glu Met Arg Thr Thr Gln Leu Gly Pro
            170                 175                 180
ggg cgc ttc caa atg acc cag gag gtg gtc tgc gac gaa tgc cct aat     751
Gly Arg Phe Gln Met Thr Gln Glu Val Val Cys Asp Glu Cys Pro Asn
        185                 190                 195
gtc aaa cta gtg aat gaa gaa cga acg ctg gaa gta gaa ata gag cct     799
Val Lys Leu Val Asn Glu Glu Arg Thr Leu Glu Val Glu Ile Glu Pro
    200                 205                 210
ggg gtg aga gac ggc atg gag tac ccc ttt att gga gaa ggt gag cct     847
Gly Val Arg Asp Gly Met Glu Tyr Pro Phe Ile Gly Glu Gly Glu Pro
215                 220                 225                 230
cac gtg gat ggg gag cct gga gat tta cgg ttc cga atc aaa gtt gtc     895
His Val Asp Gly Glu Pro Gly Asp Leu Arg Phe Arg Ile Lys Val Val
                235                 240                 245
aag cac cca ata ttt gaa agg aga gga gat gat ttg tac aca aat gtg     943
Lys His Pro Ile Phe Glu Arg Arg Gly Asp Asp Leu Tyr Thr Asn Val
            250                 255                 260
aca atc tca tta gtt gag tca ctg gtt ggc ttt gag atg gat att act     991
Thr Ile Ser Leu Val Glu Ser Leu Val Gly Phe Glu Met Asp Ile Thr
        265                 270                 275
cac ttg gat ggt cac aag gta cat att tcc cgg gat aag atc acc agg    1039
```



```
His Leu Asp Gly His Lys Val His Ile Ser Arg Asp Lys Ile Thr Arg
    280                 285                 290
cca gga gcg aag cta tgg aag aaa ggg gaa ggg ctc ccc aac ttt gac    1087
Pro Gly Ala Lys Leu Trp Lys Lys Gly Glu Gly Leu Pro Asn Phe Asp
295                 300                 305                 310
aac aac aat atc aag ggc tct ttg ata atc act ttt gat gtg gat ttt    1135
Asn Asn Asn Ile Lys Gly Ser Leu Ile Ile Thr Phe Asp Val Asp Phe
                315                 320                 325
cca aaa gaa cag tta aca gag gaa gcg aga gaa ggt atc aaa cag cta    1183
Pro Lys Glu Gln Leu Thr Glu Glu Ala Arg Glu Gly Ile Lys Gln Leu
            330                 335                 340
ctg aaa caa ggg tca gtg cag aag gta tac aat gga ctg caa gga tat    1231
Leu Lys Gln Gly Ser Val Gln Lys Val Tyr Asn Gly Leu Gln Gly Tyr
        345                 350                 355
tgagagtga ataaaattgg actttgttta aaataagtga ataagcgata tttattatct   1290
gcaaggtttt tttgtgtgtg tttttgtttt tattttcaat atgcaagtta ggcttaattt   1350
ttttatctaa tgatcatcat gaaatgaata agagggctta agaatttgtc catttgcatt   1410
cggaaaagaa tgaccagcaa aaggtttact aatacctctc cctttgggga tttaatgtct   1470
ggtgctgccg cctgagtttc aagaattaaa gctgcaagag gactccagga gcaaaagaaa   1530
cacaatatag agggttggag ttgttagcaa tttcattcaa aatgccaact ggagaagtct   1590
gtttttaaat acattttgtt gttatttt                                      1619

<210> 112
<211> 2054
<212> DNA
<213> Homo Sapience
<220>
<221> CDS
<222> (254)...(934)

<400> 112
cacatggcca agtccgcccc gccccctccc cgtccccgcc gctgcagcgg tcgccttcgg     60
agcgaagggt accgacccgg cagaagctcg gagctctcgg ggtatcgagg aggcaggccc    120
gcgggcgcac gggcgagcgg gccgggagcc ggagcggcgg aggagccggc agcagcggcg    180
cggcgggctc caggcgaggc ggtcgacgct cctgaaaact tgcgcgcgcg ctcgcgccac    240
```

```
tgcgcccgga gcg atg aag atg gtc gcg ccc tgg acg cgg ttc tac tcc      289
               Met Lys Met Val Ala Pro Trp Thr Arg Phe Tyr Ser
                1               5                   10
aac agc tgc tgc ttg tgc tgc cat gtc cgc acc ggc acc atc ctg ctc     337
Asn Ser Cys Cys Leu Cys Cys His Val Arg Thr Gly Thr Ile Leu Leu
        15                  20                  25
ggc gtc tgg tat ctg atc atc aat gct gtg gta ctg ttg att tta ttg     385
Gly Val Trp Tyr Leu Ile Ile Asn Ala Val Val Leu Leu Ile Leu Leu
    30                  35                  40
agt gcc ctg gct gat ccg gat cag tat aac ttt tca agt tct gaa ctg     433
Ser Ala Leu Ala Asp Pro Asp Gln Tyr Asn Phe Ser Ser Ser Glu Leu
45                  50                  55                  60
gga ggt gac ttt gag ttc atg gat gat gcc aac atg tgc att gcc att     481
Gly Gly Asp Phe Glu Phe Met Asp Asp Ala Asn Met Cys Ile Ala Ile
                65                  70                  75
gcg att tct ctt ctc atg atc ctg ata tgt gct atg gct act tac gga     529
Ala Ile Ser Leu Leu Met Ile Leu Ile Cys Ala Met Ala Thr Tyr Gly
            80                  85                  90
gcg tac aag caa cgc gca gcc tgg atc atc cca ttc ttc tgt tac cag     577
Ala Tyr Lys Gln Arg Ala Ala Trp Ile Ile Pro Phe Phe Cys Tyr Gln
        95                  100                 105
atc ttt gac ttt gcc ctg aac atg ttg gtt gca atc act gtg ctt att     625
Ile Phe Asp Phe Ala Leu Asn Met Leu Val Ala Ile Thr Val Leu Ile
    110                 115                 120
tat cca aac tcc att cag gaa tac ata cgg caa ctg cct cct aat ttt     673
Tyr Pro Asn Ser Ile Gln Glu Tyr Ile Arg Gln Leu Pro Pro Asn Phe
125                 130                 135                 140
ccc tac aga gat gat gtc atg tca gtg aat cct acc tgt ttg gtc ctt     721
Pro Tyr Arg Asp Asp Val Met Ser Val Asn Pro Thr Cys Leu Val Leu
                145                 150                 155
att att ctt ctg ttt att agc att atc ttg act ttt aag ggt tac ttg     769
Ile Ile Leu Leu Phe Ile Ser Ile Ile Leu Thr Phe Lys Gly Tyr Leu
            160                 165                 170
att agc tgt gtt tgg aac tgc tac cga tac atc aat ggt agg aac tcc     817
Ile Ser Cys Val Trp Asn Cys Tyr Arg Tyr Ile Asn Gly Arg Asn Ser
```



```
        175                 180                 185
tct gat gtc ctg gtt tat gtt acc agc aat gac act acg gtg ctg cta     865
Ser Asp Val Leu Val Tyr Val Thr Ser Asn Asp Thr Thr Val Leu Leu
    190                 195                 200
ccc ccg tat gat gat gcc act gtg aat ggt gct gcc aag gag cca ccg     913
Pro Pro Tyr Asp Asp Ala Thr Val Asn Gly Ala Ala Lys Glu Pro Pro
205                 210                 215                 220
cca cct tac gtg tct gcc taagccttca agtgggcgga gctgagggc             960
Pro Pro Tyr Val Ser Ala
                225
agcagcttga ctttgcagac atctgagcaa tagttctgtt atttcacttt tgccatgagc   1020
ctctctgagc ttgtttgttg ctgaaatgct actttttaaa atttagatgt tagattgaaa   1080
actgtagttt tcaacatatg ctttgctgga acactgtgat agattaactg tagaattctt   1140
cctgtacgat tggggatata atgggcttca ctaaccttcc ctaggcattg aaacttcccc   1200
caaatctgat ggacctagaa gtctgctttt gtacctgctg ggccccaaag ttgggcattt   1260
ttctctctgt tccctctctt ttgaaaatgt aaaataaaac caaaaataga caactttttc   1320
ttcagccatt ccagcataga gaacaaaacc ttatggaaac aggaatgtca attgtgtaat   1380
cattgttcta attaggtaaa tagaagtcct tatgtatgtg ttacaagaat ttcccccaca   1440
acatccttta tgactgaagt tcaatgacag tttgtgtttg gtggtaaagg attttctcca   1500
tggcctgaat taagaccatt agaaagcacc aggccgtggg agcagtgacc atctgctgac   1560
tgttcttgtg gatcttgtgt ccagggacat ggggtgacat gcctcgtatg tgttagaggg   1620
tggaatggat gtgtttggcg ctgcatggga tctggtgccc ctcttctcct ggattcacat   1680
ccccacccag ggcccgcttt tactaagtgt tctgccctag attggttcaa ggaggtcatc   1740
caactgactt tatcaagtgg aattgggata tatttgatat acttctgcct aacaacatgg   1800
aaaagggttt tcttttccct gcaagctaca tcctactgct ttgaacttcc aagtatgtct   1860
agtcaccttt taaaatgtaa acattttcag aaaaatgagg attgccttcc ttgtatgcgc   1920
tttttacctt gactacctga attgcaaggg atttttatat attcatatgt tacaaagtca   1980
gcaactctcc tgttggttca ttattgaatg tgctgtaaat taagttgttt gcaattaaaa   2040
caaggtttgc ccac                                                     2054
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<210> 113

<211> 1380

<212> DNA

<213> Homo Sapience

<220>

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<221> CDS
<222> (43)...(630)

<400> 113
gcagtctgtc tgagggcggc cgaagtggct ggctcattta ag atg agg ctt ctg      54
                                               Met Arg Leu Leu
                                                 1
ctg ctt ctc cta gtg gcg gcg tct gcg atg gtc cgg agc gag gcc tcg    102
Leu Leu Leu Leu Val Ala Ala Ser Ala Met Val Arg Ser Glu Ala Ser
  5                  10                  15                  20
gcc aat ctg ggc ggc gtg ccc agc aag aga tta aag atg cag tac gcc    150
Ala Asn Leu Gly Gly Val Pro Ser Lys Arg Leu Lys Met Gln Tyr Ala
                 25                  30                  35
acg ggg ccg ctg ctc aag ttc cag att tgt gtt tcc tga ggt tat agg    198
Thr Gly Pro Leu Leu Lys Phe Gln Ile Cys Val Ser Xaa Gly Tyr Arg
             40                  45                  50
cgg gtg ttt gag gag tac atg cgg gtt att agc cag cgg tac cca gac    246
Arg Val Phe Glu Glu Tyr Met Arg Val Ile Ser Gln Arg Tyr Pro Asp
         55                  60                  65
atc cgc att gaa gga gag aat tac ctc cct caa cca ata tat aga cac    294
Ile Arg Ile Glu Gly Glu Asn Tyr Leu Pro Gln Pro Ile Tyr Arg His
     70                  75                  80
ata gca tct ttc ctg tca gtc ttc aaa cta gta tta ata ggc tta ata    342
Ile Ala Ser Phe Leu Ser Val Phe Lys Leu Val Leu Ile Gly Leu Ile
 85                  90                  95                 100
att gtt ggc aag gat cct ttt gct ttc ttt ggc atg caa gct cct agc    390
Ile Val Gly Lys Asp Pro Phe Ala Phe Phe Gly Met Gln Ala Pro Ser
                105                 110                 115
atc tgg cag tgg ggc caa gaa aat aag gtt tat gca tgt atg atg gtt    438
Ile Trp Gln Trp Gly Gln Glu Asn Lys Val Tyr Ala Cys Met Met Val
            120                 125                 130
ttc ttc ttg agc aac atg att gag aac cag tgt atg tca aca ggt gca    486
Phe Phe Leu Ser Asn Met Ile Glu Asn Gln Cys Met Ser Thr Gly Ala
        135                 140                 145
ttt gag ata act tta aat gat gta cct gtg tgg tct aag ctg gaa tct    534
```



```
Phe Glu Ile Thr Leu Asn Asp Val Pro Val Trp Ser Lys Leu Glu Ser
    150                 155                 160
ggt cac ctt cca tcc atg caa caa ctt gtt caa att ctt gac aat gaa    582
Gly His Leu Pro Ser Met Gln Gln Leu Val Gln Ile Leu Asp Asn Glu
165                 170                 175                 180
atg aag ctc aat gtg cat atg gat tca atc cca cac cat cga tca        627
Met Lys Leu Asn Val His Met Asp Ser Ile Pro His His Arg Ser
                185                 190                 195
tag caccacctat cagcactgaa aactcttttg cattaaggga tcattgcaag         680
agcagcgtga ctgacattat gaaggcctgt actgaagaca gcaagctgtt agtacagacc  740
agatgctttc ttggcaggct cgttgtacct cttggaaaac ctcaatgcaa gatagtgttt  800
cagtgctggc atatttgga attctgcaca ttcatggagt gcaataatac tgtatagctt   860
tccccacctc ccacaaaatc acccagttaa tgtgtgtgtg tgttttttt tttaaggtaa   920
acattactac ttgtaacttt ttttcttagt catatttgaa aaagtagaaa attgagttac  980
aatttgattt tttttccaaa gatgtctgtt aaatctgttg tgcttttata tgaatatttg 1040
ttttttatag tttaaaattg atcctttggg aatccagttg aagttcccaa atactttata 1100
agagtttatc agacatctct aatttggcca tgtccagttt atacagttta caaaatatag 1160
cagatgcaag attatggggg aaatcctata ttcagagtac tctataaatt tttgtgtatg 1220
tgtgtatgtg cgtgtgatta ccagagaact actaaaaaaa ccaactgctt tttaaatcct 1280
attgtgtagt taaagtgtca tgccttgacc aatctaatga attgattaat taactgggcc 1340
tttatactta actaaataaa aaactaagca gatatgagtt                       1380

<210> 114
<211> 1292
<212> DNA
<213> Homo Sapience
<220>
<221> CDS
<222> (113)...(1132)

<400> 114
aaaagtgcgg ctctgggctg gccgaagggg tggcgctgcg atcccgcagg gcagcgacgc   60
gactctggtg cgggccgtct tcttcccccc gagctgggcg tgcgcggccg ca atg aac 118
                                                          Met Asn
                                                            1
```

tgg gag ctg ctg ctg tgg ctg ctg gtg ctg tgc gcg ctg ctc ctg ctc 166
Trp Glu Leu Leu Leu Trp Leu Leu Val Leu Cys Ala Leu Leu Leu Leu
5 10 15
ttg gtg cag ctg ctg cgc ttc ctg agg gct gac ggc gac ctg acg cta 214
Leu Val Gln Leu Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu Thr Leu
20 25 30
cta tgg gcc gag tgg cag gga cga cgc cca gaa tgg gag ctg act gat 262
Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu Thr Asp
35 40 45 50
atg gtg gtg tgg gtg act gga gcc tcg agt gga att ggt gag gag ctg 310
Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu Glu Leu
55 60 65
gct tac cag ttg tct aaa cta gga gtt tct ctt gtg ctg tca gcc aga 358
Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser Ala Arg
70 75 80
aga gtg cat gag ctg gaa agg gtg aaa aga aga tgc cta gag aat ggc 406
Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu Glu Asn Gly
85 90 95
aat tta aaa gaa aaa gat ata ctt gtt ttg ccc ctt gac ctg acc gac 454
Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu Asp Leu Thr Asp
100 105 110
act ggt tcc cat gaa gcg gct acc aaa gct gtt ctc cag gag ttt ggt 502
Thr Gly Ser His Glu Ala Ala Thr Lys Ala Val Leu Gln Glu Phe Gly
115 120 125 130
aga atc gac att ctg gtc aac aat ggt gga atg tcc cag cgt tct ctg 550
Arg Ile Asp Ile Leu Val Asn Asn Gly Gly Met Ser Gln Arg Ser Leu
135 140 145
tgc atg gat acc agc ttg gat gtc tac aga aag cta ata gag ctt aac 598
Cys Met Asp Thr Ser Leu Asp Val Tyr Arg Lys Leu Ile Glu Leu Asn
150 155 160
tac tta ggg acg gtg tcc ttg aca aaa tgt gtt ctg cct cac atg atc 646
Tyr Leu Gly Thr Val Ser Leu Thr Lys Cys Val Leu Pro His Met Ile
165 170 175
gag agg aag caa gga aag att gtt act gtg aat agc atc ctg ggt atc 694
Glu Arg Lys Gln Gly Lys Ile Val Thr Val Asn Ser Ile Leu Gly Ile

180 185 190
ata tct gta cct ctt tcc att gga tac tgt gct agc aag cat gct ctc 742
Ile Ser Val Pro Leu Ser Ile Gly Tyr Cys Ala Ser Lys His Ala Leu
195 200 205 210
cgg ggt ttt ttt aat ggc ctt cga aca gaa ctt gcc aca tac cca ggt 790
Arg Gly Phe Phe Asn Gly Leu Arg Thr Glu Leu Ala Thr Tyr Pro Gly
215 220 225
ata ata gtt tct aac att tgc cca gga cct gtg caa tca aat att gtg 838
Ile Ile Val Ser Asn Ile Cys Pro Gly Pro Val Gln Ser Asn Ile Val
230 235 240
gag aat tcc cta gct gga gaa gtc aca aag act ata ggc aat aat gga 886
Glu Asn Ser Leu Ala Gly Glu Val Thr Lys Thr Ile Gly Asn Asn Gly
245 250 255
gac cag tcc cac aag atg aca acc agt cgt tgt gtg cgg ctg atg tta 934
Asp Gln Ser His Lys Met Thr Thr Ser Arg Cys Val Arg Leu Met Leu
260 265 270
atc agc atg gcc aat gat ttg aaa gaa gtt tgg atc tca gaa caa cct 982
Ile Ser Met Ala Asn Asp Leu Lys Glu Val Trp Ile Ser Glu Gln Pro
275 280 285 290
ttc ttg tta gta aca tat ttg tgg caa tac atg cca acc tgg gcc tgg 1030
Phe Leu Leu Val Thr Tyr Leu Trp Gln Tyr Met Pro Thr Trp Ala Trp
295 300 305
tgg ata acc aac aag atg ggg aag aaa agg att gag aac ttt aag agt 1078
Trp Ile Thr Asn Lys Met Gly Lys Lys Arg Ile Glu Asn Phe Lys Ser
310 315 320
ggt gtg gat gca gac tct tct tat ttt aaa atc ttt aag aca aaa cat 1126
Gly Val Asp Ala Asp Ser Ser Tyr Phe Lys Ile Phe Lys Thr Lys His
325 330 335
gac tgaaaagagc atctgtactt ttcaagccac tggagggaaa aatggaaaac a 1180
Asp

tgaaaacagc aatcttctta tgcttctgaa taatcaaaga ctaatttgtg gttttacttt 1240
ttaatagata tgactttgct tccaacatgg aatgaaataa aaaataagta at 1292

<210> 115

<211> 2168
<212> DNA
<213> Homo Sapience
<220>
<221> CDS
<222> (56)...(1519)

<400> 115

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tttccgccgc cgcctgggag gggacccggg ctgccaggcg cccagctgtg cccag        55
atg gat ggg aca gag acc cgg cag cgg agg ctg gac agc tgt ggc aag    103
Met Asp Gly Thr Glu Thr Arg Gln Arg Arg Leu Asp Ser Cys Gly Lys
  1               5                  10                  15
cca ggg gag ctg ggg ctt cct cac ccc ctc agc aca gga gga ctc cct    151
Pro Gly Glu Leu Gly Leu Pro His Pro Leu Ser Thr Gly Gly Leu Pro
             20                  25                  30
gta gcc tca gaa gat gga gct ctc agg gcc cct gag agc caa agc gtg    199
Val Ala Ser Glu Asp Gly Ala Leu Arg Ala Pro Glu Ser Gln Ser Val
         35                  40                  45
acc ccc aag cca ctg gag act gag cct agc agg gag acc gcc tgg tcc    247
Thr Pro Lys Pro Leu Glu Thr Glu Pro Ser Arg Glu Thr Ala Trp Ser
     50                  55                  60
ata ggc ctt cag gtg acc gtg ccc ttc atg ttt gca ggc ctg gga ctg    295
Ile Gly Leu Gln Val Thr Val Pro Phe Met Phe Ala Gly Leu Gly Leu
 65                  70                  75                  80
tcc tgg gcc ggc atg ctt ctg gac tat ttc cag cac tgg cct gtg ttt    343
Ser Trp Ala Gly Met Leu Leu Asp Tyr Phe Gln His Trp Pro Val Phe
                 85                  90                  95
gtg gag gtg aaa gac ctt ttg aca ttg gtg ccg ccc ctg gtg ggc ctg    391
Val Glu Val Lys Asp Leu Leu Thr Leu Val Pro Pro Leu Val Gly Leu
            100                 105                 110
aag ggg aac ctg gag atg aca ctg gca tcc aga ctc tcc aca gct gcc    439
Lys Gly Asn Leu Glu Met Thr Leu Ala Ser Arg Leu Ser Thr Ala Ala
        115                 120                 125
aac act gga caa att gat gac ccc cag gag cag cac aga gtc atc agc    487
Asn Thr Gly Gln Ile Asp Asp Pro Gln Glu Gln His Arg Val Ile Ser
```



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    130                 135                 140
agc aac ctg gcc ctc atc cag gtg cag gcc act gtc gtg ggg ctc ttg    535
Ser Asn Leu Ala Leu Ile Gln Val Gln Ala Thr Val Val Gly Leu Leu
145                 150                 155                 160
gct gct gtg gct gcg ctg ctg ttg ggc gtg gtg tct cga gag gaa gtg    583
Ala Ala Val Ala Ala Leu Leu Leu Gly Val Val Ser Arg Glu Glu Val
                165                 170                 175
gat gtc gcc aag gtg gag ttg ctg tgt gcc agc agt gtc ctc act gcc    631
Asp Val Ala Lys Val Glu Leu Leu Cys Ala Ser Ser Val Leu Thr Ala
            180                 185                 190
ttc ctt gca gcc ttt gcc ctg ggg gtg ctg atg gtc tgt ata gtg att    679
Phe Leu Ala Ala Phe Ala Leu Gly Val Leu Met Val Cys Ile Val Ile
        195                 200                 205
ggt gct cga aag ctc ggg gtc aac cca gac aac att gcc acg ccc att    727
Gly Ala Arg Lys Leu Gly Val Asn Pro Asp Asn Ile Ala Thr Pro Ile
    210                 215                 220
gca gcc agc ctg gga gac ctc atc aca ctg tcc att ctg gct ttg gtt    775
Ala Ala Ser Leu Gly Asp Leu Ile Thr Leu Ser Ile Leu Ala Leu Val
225                 230                 235                 240
agc agc ttc ttc tac aga cac aaa gat agt cgg tat ctg acg ccg ctg    823
Ser Ser Phe Phe Tyr Arg His Lys Asp Ser Arg Tyr Leu Thr Pro Leu
                245                 250                 255
gtc tgc ctc agc ttt gcg gct ctg acc cca gtg tgg gtc ctc att gcc    871
Val Cys Leu Ser Phe Ala Ala Leu Thr Pro Val Trp Val Leu Ile Ala
            260                 265                 270
aag cag agc cca ccc atc gtg aag atc ctg aag ttt ggc tgg ttc cca    919
Lys Gln Ser Pro Pro Ile Val Lys Ile Leu Lys Phe Gly Trp Phe Pro
        275                 280                 285
atc atc ctg gcc atg gtc atc agc agt ttc gga gga ctc atc ttg agc    967
Ile Ile Leu Ala Met Val Ile Ser Ser Phe Gly Gly Leu Ile Leu Ser
    290                 295                 300
aaa acc gtt tct aaa cag cag tac aaa ggc atg gcg ata ttt acc ccc   1015
Lys Thr Val Ser Lys Gln Gln Tyr Lys Gly Met Ala Ile Phe Thr Pro
305                 310                 315                 320
gtc ata tgt ggt gtt ggt ggc aat ctg gtg gcc att cag acc agc cga   1063
```

```
Val Ile Cys Gly Val Gly Gly Asn Leu Val Ala Ile Gln Thr Ser Arg
            325                 330                 335
atc tca acc tac ctg cac atg tgg agt gca cct ggc gtc ctg ccc ctc     1111
Ile Ser Thr Tyr Leu His Met Trp Ser Ala Pro Gly Val Leu Pro Leu
        340                 345                 350
cag atg aag aaa ttc tgg ccc aac ccg tgt tct act ttc tgc acg tca     1159
Gln Met Lys Lys Phe Trp Pro Asn Pro Cys Ser Thr Phe Cys Thr Ser
    355                 360                 365
gaa atc aat tcc atg tca gct cga gtc ctg ctc ttg ctg gtg gtc cca     1207
Glu Ile Asn Ser Met Ser Ala Arg Val Leu Leu Leu Leu Val Val Pro
    370                 375                 380
ggc cat ctg att ttc ttc tac atc atc tac ctg gtg gag ggt cag tca     1255
Gly His Leu Ile Phe Phe Tyr Ile Ile Tyr Leu Val Glu Gly Gln Ser
385                 390                 395                 400
gtc ata aac agc cag acc ttt gtg gtg ctc tac ctg ctg gca ggc ctg     1303
Val Ile Asn Ser Gln Thr Phe Val Val Leu Tyr Leu Leu Ala Gly Leu
                405                 410                 415
atc cag gtg aca atc ctg ctg tac ctg gca gaa gtg atg gtt cgg ctg     1351
Ile Gln Val Thr Ile Leu Leu Tyr Leu Ala Glu Val Met Val Arg Leu
            420                 425                 430
act tgg cac cag gcc ctg gat cct gac aac cac tgc atc ccc tac ctt     1399
Thr Trp His Gln Ala Leu Asp Pro Asp Asn His Cys Ile Pro Tyr Leu
        435                 440                 445
aca ggg ctg ggg gac ctg ctc ggt act ggc ctc ctg gca ctc tgc ttt     1447
Thr Gly Leu Gly Asp Leu Leu Gly Thr Gly Leu Leu Ala Leu Cys Phe
    450                 455                 460
ttc act gac tgg cta ctg aag agc aag gca gag ctg ggt ggc atc tca     1495
Phe Thr Asp Trp Leu Leu Lys Ser Lys Ala Glu Leu Gly Gly Ile Ser
465                 470                 475                 480
gaa ctg gca tct gga cct ccc taactgggcc ccgctggtcc catttgctca ttag   1550
Glu Leu Ala Ser Gly Pro Pro
                485
aatttcctct cacatcagtg ggatacagaa ttcagtttct cccttgccag gtccttggga   1610
tggttgaccc ctgcctctgc agtagccttt tgtgagtctg ctaaggtagc tctcacacac   1670
ctcggctctg ggttgatac ctgagcctgc aatagagccc tgaaatcaag agcatggctt    1730
```



```
gagtgtgtga atatgatgtg tgcacatgct taatgagcgt gcaagtgtgc acacgtttgt   1790
ggagaggagg gtgttctggc ctgagaagct aaagaagagg catgtccagt atgctttgca   1850
gggtgtgttt gctcttttcc atgcccatgc aacccagatt ggggtggagc aggaaggagc   1910
tcttttctgt tcccaagcct cagaactctt gagctgtggc ttacttgctg tcttcaccag   1970
gttcaagctc cgtgggccac actgctgctg tgccaagaag gtgtacagcc tccccaggat   2030
ggggcctcat acaacccttc atctgcactc aacatttaat cgtgtccttg ctgtcttttt   2090
atttcctttt ttgttagcaa aaacctctat ttagatttca ataatcagag aagtgtaaaa   2150
taaaacagat tatattgt                                                 2168
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<210> 116
<211> 1357
<212> DNA
<213> Homo Sapience
<220>
<221> CDS
<222> (81)...(1262)

<400> 116

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cgtgcgtttg tggccgtccg gcctccctga catgcagccc tctggacccc gaggttggac    60
cctactgtga cacacctacc atg cgg aca ctc ttc aac ctc ctc tgg ctt      110
                      Met Arg Thr Leu Phe Asn Leu Leu Trp Leu
                        1               5                  10
gcc ctg gcc tgc agc cct gtt cac act acc ctg tca aag tca gat gcc     158
Ala Leu Ala Cys Ser Pro Val His Thr Thr Leu Ser Lys Ser Asp Ala
                15                  20                  25
aaa aaa gcc gcc tca aag acg ctg ctg gag aag agt cag ttt tca gat     203
Lys Lys Ala Ala Ser Lys Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp
            30                  35                  40
aag ccg gtg caa gac cgg ggt ttg gtg gtg acg gac ctc aaa gct gag     254
Lys Pro Val Gln Asp Arg Gly Leu Val Val Thr Asp Leu Lys Ala Glu
        45                  50                  55
agt gtg gtt ctt gag cat cgc agc tac tgc tcg gca aag gcc cgg gac     302
Ser Val Val Leu Glu His Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp
    60                  65                  70
aga cac ttt gct ggg gat gta ctg ggc tat gtc act cca tgg aac agc     350
```

```
Arg His Phe Ala Gly Asp Val Leu Gly Tyr Val Thr Pro Trp Asn Ser
 75                  80                  85                  90
cat ggc tac gat gtc acc aag gtc ttt ggg agc aag ttc aca cag atc      398
His Gly Tyr Asp Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile
                 95                 100                 105
tca ccc gtc tgg ctg cag ctg aag aga cgt ggc cgt gag atg ttt gag      446
Ser Pro Val Trp Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu
            110                 115                 120
gtc acg ggc ctc cac gac gtg gac caa ggg tgg atg cga gct gtc agg      494
Val Thr Gly Leu His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg
        125                 130                 135
aag cat gcc aag ggc ctg cac ata gtg cct cgg ctc ctg ttt gag gac      542
Lys His Ala Lys Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp
    140                 145                 150
tgg act tac gat gat ttc cgg aac gtc tta gac agt gag gat gag ata      590
Trp Thr Tyr Asp Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile
155                 160                 165                 170
gag gag ctg agc aag acc gtg gtc cag gtg gca aag aac cag cat ttc      638
Glu Glu Leu Ser Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe
                175                 180                 185
gat ggc ttc gtg gtg gag gtc tgg aac cag ctg cta agc cag aag cgc      686
Asp Gly Phe Val Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg
            190                 195                 200
gtg ggc ctc atc cac atg ctc acc cac ttg gcc gag gct ctg cac cag      734
Val Gly Leu Ile His Met Leu Thr His Leu Ala Glu Ala Leu His Gln
        205                 210                 215
gcc cgg ctg ctg gcc ctc ctg gtc atc ccg cct gcc atc acc ccc ggg      782
Ala Arg Leu Leu Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly
    220                 225                 230
acc gac cag ctg ggc atg ttc acg cac aag gag ttt gag cag ctg gcc      830
Thr Asp Gln Leu Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala
235                 240                 245                 250
ccc gtg ctg gat ggt ttc agc ctc atg acc tac gac tac tct aca gcg      878
Pro Val Leu Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala
                255                 260                 265
```



```
cat cag cct ggc cct aat gca ccc ctg tcc tgg gtt cga gcc tgc gtc      926
His Gln Pro Gly Pro Asn Ala Pro Leu Ser Trp Val Arg Ala Cys Val
            270                 275                 280
cag gtc ctg gac ccg aag tcc aag tgg cga agc aaa atc ctc ctg ggg      974
Gln Val Leu Asp Pro Lys Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly
        285                 290                 295
ctc aac ttc tat ggt atg gac tac gcg acc tcc aag gat gcc cgt gag     1022
Leu Asn Phe Tyr Gly Met Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu
    300                 305                 310
cct gtt gtc ggg gcc agg tac atc cag aca ctg aag gac cac agg ccc     1070
Pro Val Val Gly Ala Arg Tyr Ile Gln Thr Leu Lys Asp His Arg Pro
315                 320                 325                 330
cgg atg gtg tgg gac agc cag gcc tca gag cac ttc ttc gag tac aag     1118
Arg Met Val Trp Asp Ser Gln Ala Ser Glu His Phe Phe Glu Tyr Lys
                335                 340                 345
aag agc cgc agt ggg agg cac gtc gtc ttc tac cca acc ctg aag tcc     1166
Lys Ser Arg Ser Gly Arg His Val Val Phe Tyr Pro Thr Leu Lys Ser
            350                 355                 360
ctg cag gtg cgg ctg gag ctg gcc cgg gag ctg ggc gtt ggg gtc tct     1214
Leu Gln Val Arg Leu Glu Leu Ala Arg Glu Leu Gly Val Gly Val Ser
        365                 370                 375
atc tgg gag ctg ggc cag ggc ctg gac tac ttc tac gac ctg ctc t       1260
Ile Trp Glu Leu Gly Gln Gly Leu Asp Tyr Phe Tyr Asp Leu Leu
    380                 385                 390
aggtgggcat tgcggcctcc gcggtggacg tgttcttttc taagccatgg agtgagtgag   1320
caggtgtgaa atacaggcct ccactccgtt tgctgtg                             1357

<210> 117
<211> 711
<212> DNA
<213> Homo Sapience
<220>
<221> CDS
<222> (8)...(598)
```

```
<400> 117
aaaggcg atg tgg agg gtg ccc ggc aca acc aga cgc cca gtc aca ggc      49
        Met Trp Arg Val Pro Gly Thr Thr Arg Arg Pro Val Thr Gly
          1               5                  10
gag agc cct ggg atg cac cgg cca gag gcc atg ctg ctg ctg ctc acg      97
Glu Ser Pro Gly Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr
 15                  20                  25                  30
ctt gcc ctc ctg ggg ggc ccc acc tgg gca ggg aag atg tat ggc cct     145
Leu Ala Leu Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro
                 35                  40                  45
gga gga ggc aag tat ttc agc acc act gaa gac tac gac cat gaa atc     193
Gly Gly Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile
             50                  55                  60
aca ggg ctg cgg gtg tct gta ggt ctt ctc ctg gtg aaa agt gtc cag     241
Thr Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln
         65                  70                  75
gtg aaa ctt gga gac tcc tgg gac gtg aaa ctg gga gcc tta ggt ggg     289
Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly Gly
     80                  85                  90
aat acc cag gaa gtc acc ctg cag cca ggc gaa tac atc aca aaa gtc     337
Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr Lys Val
 95                 100                 105                 110
ttt gtc gcc ttc caa gct ttc ctc cgg ggt atg gtc atg tac acc agc     385
Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met Tyr Thr Ser
                115                 120                 125
aag gac cgc tat ttc tat ttt ggg aag ctt gat ggc cag atc tcc tct     433
Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly Gln Ile Ser Ser
            130                 135                 140
gcc tac ccc agc caa gag ggg cag gtg ctg gtg ggc atc tat ggc cag     481
Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val Gly Ile Tyr Gly Gln
        145                 150                 155
tat caa ctc ctt ggc atc aag agc att ggc ttt gaa tgg aat tat cca     529
Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly Phe Glu Trp Asn Tyr Pro
    160                 165                 170
cta gag gag ccg acc act gag cca cca gtt aat ctc aca tac tca gca     577
```



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Leu Glu Glu Pro Thr Thr Glu Pro Pro Val Asn Leu Thr Tyr Ser Ala
175                 180                 185                 190
aac tca ccc gtg ggt cgc tagggtgggg tatggggcca tccgagctga ggcca      630
Asn Ser Pro Val Gly Arg
                195
tctgtgtggt ggtggctgat ggtactggag taactgagtc gggacgctga atctgaatcc   690
accaataaat aaagcttctg c                                             711

<210> 118
<211> 651
<212> DNA
<213> Homo Sapience
<220>
<221> CDS
<222> (242)...(565)

<400> 118
aaagaaacaa gccgggggac tgcgagccag ggactcgggc cgcggggcgg gaagaagtgg    60
ggcagcgctt ggccaggccg aaaggacttt gggggtgggg gctgggagtc cgtgtctcga   120
atgagggagg agaggtggag ttgccggggc tcaggcccgg cctcgagcat gggcggatga   180
gaggagtcgg gagccgaggc ctagggtcct tcgggtgagg ggagacggag ccagcgagga   240
g atg gag cag aag ctt gtg gag gag att ctt caa gca atc act atg       286
  Met Glu Gln Lys Leu Val Glu Glu Ile Leu Gln Ala Ile Thr Met
    1               5                  10                  15
tca aca gac aca ggt gtt tcc ctt cct tca tat gag gaa gat cag gga     334
Ser Thr Asp Thr Gly Val Ser Leu Pro Ser Tyr Glu Glu Asp Gln Gly
                 20                  25                  30
tca aaa ctc att cga aaa gct aaa gag gca cca ttc gta ccc gtt gga     382
Ser Lys Leu Ile Arg Lys Ala Lys Glu Ala Pro Phe Val Pro Val Gly
             35                  40                  45
ata gcg ggt ttt gca gca att gtt gca tat gga tta tat aaa ctg aag     430
Ile Ala Gly Phe Ala Ala Ile Val Ala Tyr Gly Leu Tyr Lys Leu Lys
         50                  55                  60
agc agg gga aat act aaa atg tcc att cat ctg atc cac atg cgt gtg     478
Ser Arg Gly Asn Thr Lys Met Ser Ile His Leu Ile His Met Arg Val
```

```
        65                  70                  75
gca gcc caa ggc ttt gtt gta gga gca atg act gtt ggt atg ggc tat       526
Ala Ala Gln Gly Phe Val Val Gly Ala Met Thr Val Gly Met Gly Tyr
 80                  85                  90                  95
tcc atg tat cgg gaa ttc tgg gca aaa cct aag cct tagaagaa              570
Ser Met Tyr Arg Glu Phe Trp Ala Lys Pro Lys Pro
                100                 105
gagatgctgt cttggtcttg ttggaggagc ttgctttagt tagatgtctt attattaaag    630
ttacctatta ttgttggaaa t                                               651

<210> 119
<211> 1310
<212> DNA
<213> Homo Sapience
<220>
<221> CDS
<222> (78)...(1130)

<400> 119
cgaacgccaa ggcggccacg tcctgctccc cctggtgaag aagctgccct gggcttgtcg     60
tcctagggtc tccagac atg tct gag gtg aag agc cgg aag aag tcg ggg        110
                   Met Ser Glu Val Lys Ser Arg Lys Lys Ser Gly
                    1               5                  10
ccc aag gga gcc cct gct gcg gag ccc ggg aag cgg agc gag ggc ggg       158
Pro Lys Gly Ala Pro Ala Ala Glu Pro Gly Lys Arg Ser Glu Gly Gly
            15                  20                  25
aag acc ccc gtg gcc cgg agc agc gga ggc ggg ggc tgg gca gac ccc       206
Lys Thr Pro Val Ala Arg Ser Ser Gly Gly Gly Gly Trp Ala Asp Pro
        30                  35                  40
cga acg tgc ctg agc ctg ctg tcg ctg ggg acg tgc ctg ggc ctg gcc       254
Arg Thr Cys Leu Ser Leu Leu Ser Leu Gly Thr Cys Leu Gly Leu Ala
    45                  50                  55
tgg ttt gta ttt cag cag tca gaa aaa ttt gca aag gtg gaa aac caa       302
Trp Phe Val Phe Gln Gln Ser Glu Lys Phe Ala Lys Val Glu Asn Gln
60                  65                  70                  75
```



```
tac cag tta ctg aaa cta gaa acc aat gaa ttc caa caa ctt caa agt       350
Tyr Gln Leu Leu Lys Leu Glu Thr Asn Glu Phe Gln Gln Leu Gln Ser
                80                  85                  90
aaa atc agt tta att tca gaa aag tgg cag aaa tct gaa gct atc atg       398
Lys Ile Ser Leu Ile Ser Glu Lys Trp Gln Lys Ser Glu Ala Ile Met
            95                  100                 105
gaa caa ttg aag tct ttt caa ata att gct cat cta aag cgt cta cag       446
Glu Gln Leu Lys Ser Phe Gln Ile Ile Ala His Leu Lys Arg Leu Gln
        110                 115                 120
gaa gaa att aat gag gta aaa act tgg tcc aat agg ata act gaa aaa       494
Glu Glu Ile Asn Glu Val Lys Thr Trp Ser Asn Arg Ile Thr Glu Lys
    125                 130                 135
cag gat ata ctg aac aac agt ctg acg acg ctt tct caa gac att aca       542
Gln Asp Ile Leu Asn Asn Ser Leu Thr Thr Leu Ser Gln Asp Ile Thr
140                 145                 150                 155
aaa gta gac caa agt aca act tcc atg gca aaa gat gtt ggt ctc aag       590
Lys Val Asp Gln Ser Thr Thr Ser Met Ala Lys Asp Val Gly Leu Lys
                160                 165                 170
att aca agt gta aaa aca gat ata cga cgg att tca ggt tta gta act       638
Ile Thr Ser Val Lys Thr Asp Ile Arg Arg Ile Ser Gly Leu Val Thr
            175                 180                 185
gat gta ata tca ttg aca gat tct gtg caa gaa cta gaa aat aaa ata       686
Asp Val Ile Ser Leu Thr Asp Ser Val Gln Glu Leu Glu Asn Lys Ile
        190                 195                 200
gag aaa gta gaa aaa aat aca gta aaa aat ata ggt gat ctt ctt tca       734
Glu Lys Val Glu Lys Asn Thr Val Lys Asn Ile Gly Asp Leu Leu Ser
    205                 210                 215
agc agt att gat cga aca gca acg ctc cga aag aca gca tct gaa aat       782
Ser Ser Ile Asp Arg Thr Ala Thr Leu Arg Lys Thr Ala Ser Glu Asn
220                 225                 230                 235
tca caa aga att aac tct gtt aag aag acg cta acc gaa cta aag agt       830
Ser Gln Arg Ile Asn Ser Val Lys Lys Thr Leu Thr Glu Leu Lys Ser
                240                 245                 250
gac ttc gac aaa cat aca gat aga ttt cta agc tta gaa ggt gac aga       878
Asp Phe Asp Lys His Thr Asp Arg Phe Leu Ser Leu Glu Gly Asp Arg
```

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                255                 260                 265
gcc aaa gtt ctg aag aca gtg act ttt gca aat gat cta aaa cca aag        926
Ala Lys Val Leu Lys Thr Val Thr Phe Ala Asn Asp Leu Lys Pro Lys
        270                 275                 280
gtg tat aat cta aag aag gac ttt tcc cgt tta gaa cca tta gta aat        974
Val Tyr Asn Leu Lys Lys Asp Phe Ser Arg Leu Glu Pro Leu Val Asn
    285                 290                 295
gat tta aca cta cgc att ggg aga ttg gtt acc gac tta cta caa aga       1022
Asp Leu Thr Leu Arg Ile Gly Arg Leu Val Thr Asp Leu Leu Gln Arg
300                 305                 310                 315
gag aaa gaa att gct ttc tta agt gaa aaa ata tct aat tta aca ata       1070
Glu Lys Glu Ile Ala Phe Leu Ser Glu Lys Ile Ser Asn Leu Thr Ile
                320                 325                 330
gtc caa gct gag att aag gat att aaa gat gaa ata gca cac att tca       1118
Val Gln Ala Glu Ile Lys Asp Ile Lys Asp Glu Ile Ala His Ile Ser
            335                 340                 345
gat atg aat tagtttgaca ttattgagat tagactaagg taattttttt aat           1170
Asp Met Asn
        350
gggacctctc atgagaagac tggtaaatca aaaataatga tattttggag caaaagtcat     1230
tttatattta atcctatttt gtacagtaaa aataaaactt taaaacaggt tgattttcca     1290
aaataaatat gctaaaacct                                                 1310

<210> 120
<211> 1400
<212> DNA
<213> Homo Sapience
<220>
<221> CDS
<222> (233)...(556)

<400> 120
tggctgtatg ctattggagg gtggaaatca catctcctgt ttatccgtgt gcttgttagg       60
tgtcagccgc cacccccccc ccatatgcag atttactcgg catggtagtg gccagcttct      120
aacacagctg gtatttcaag tctcctggga cctcactcag gaatgatacc ccctcagtag      180
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aagcagcagg tgatcttaac tcctttcaaa gagcaggcct gtctgggaag cc atg          235
                                                          Met
                                                            1
tcc tca gca ggc aca gca acc cct ctg gaa atg gat cac aaa ctc act        283
Ser Ser Ala Gly Thr Ala Thr Pro Leu Glu Met Asp His Lys Leu Thr
            5                  10                  15
tct cag cca ggc agg cca agc ttc tat tgt aac agt agg cac agt ata        331
Ser Gln Pro Gly Arg Pro Ser Phe Tyr Cys Asn Ser Arg His Ser Ile
        20                  25                  30
gtc gga tca tca cat cag ctg ggt ttt tgg ttt agt cat cta gag tcg        379
Val Gly Ser Ser His Gln Leu Gly Phe Trp Phe Ser His Leu Glu Ser
    35                  40                  45
tct gga cta aag gtc ttt cag gtc tcc ttg ccc tgt gag tgc gtg aac        427
Ser Gly Leu Lys Val Phe Gln Val Ser Leu Pro Cys Glu Cys Val Asn
50                  55                  60                  65
ctc ccc acc cga att gcc tca gtt gtc ctg agc ctc atg tct ctc ctg        475
Leu Pro Thr Arg Ile Ala Ser Val Val Leu Ser Leu Met Ser Leu Leu
                70                  75                  80
gtg gtg ggc cag gcc cct gca tgg gaa ggg agc ctg ctg cgg ggc agg        523
Val Val Gly Gln Ala Pro Ala Trp Glu Gly Ser Leu Leu Arg Gly Arg
            85                  90                  95
cca gct ggg ggt gct cac cta tgc gca gca tgaagttatt gaaggac             570
Pro Ala Gly Gly Ala His Leu Cys Ala Ala
        100                 105
tggttgttga tgttggtgag cgtatccttc atggccagcg cgaagtcggc caggtcagcc      630
aggtgctgcc agcgctctct ctcggacttg tcttcctgtg ccaggggacc gtggagaaag      690
tgtcaggggc cgctcactgc agcagcctgc tctgctgcct tccctggcag tgttctgggg      750
gtggattccc tacacctaga tgttcaaggc cttacttttc ctccccacaaa ggagtcgcag     810
ccacgctagc tctgacttgc cactgtgaca aagttcacgt agcaggtcta ggcaaagact      870
gggcaattga gcagaggaga cggacctgtg agtctgacca cgaggcggac cccttcacct      930
tggctgggcc tggtcctggt ccttaggttt tgtcaggttg tccttgtttg gatccctcaa      990
ctaggtgata agcactggag ggggatgacc cgccttggac gtgtttcttt aacctcatcc     1050
atataatagg gccgtgggat ggttgtagag gtaaagcagg atgatggtgt tttaagacca     1110
gagcttggga ccagggctcc tacacctaat tttctctcct ggtagctgaa caaaggtcta     1170
aattagctta acaaaagaac aggctgccgt cagccagagt tctgaaggcc atgctttcag     1230
```

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tttcccttgt tgacaattgc tctccagttc ctatgaaagc acagagcctt agggggcctg   1290
gccacagaac acaaccatct taggcctgag ctgtgaacag caggggttg tgtgtctgtt   1350
ctgtttctct gcttgccgaa ctttctcaat aaaccctatt tcttatttat              1400

<210> 121
<211> 483
<212> PRT
<213> Homo sapience

<400> 121
Met Lys Ala Phe His Thr Phe Cys Val Val Leu Leu Val Phe Gly Ser
 1               5                  10                  15
Val Ser Glu Ala Lys Phe Asp Asp Phe Glu Asp Glu Glu Asp Ile Val
            20                  25                  30
Glu Tyr Asp Asp Asn Asp Phe Ala Glu Phe Glu Asp Val Met Glu Asp
        35                  40                  45
Ser Val Thr Glu Ser Pro Gln Arg Val Ile Ile Thr Glu Asp Asp Glu
    50                  55                  60
Asp Glu Thr Thr Val Glu Leu Glu Gly Gln Asp Glu Asn Gln Glu Gly
65                  70                  75                  80
Asp Phe Glu Asp Ala Asp Thr Gln Glu Gly Asp Thr Glu Ser Glu Pro
                85                  90                  95
Tyr Asp Asp Glu Glu Phe Glu Gly Tyr Glu Asp Lys Pro Asp Thr Ser
            100                 105                 110
Ser Ser Lys Asn Lys Asp Pro Ile Thr Ile Val Asp Val Pro Ala His
        115                 120                 125
Leu Gln Asn Ser Trp Glu Ser Tyr Tyr Leu Glu Ile Leu Met Val Thr
    130                 135                 140
Gly Leu Leu Ala Tyr Ile Met Asn Tyr Ile Ile Gly Lys Asn Lys Asn
145                 150                 155                 160
Ser Arg Leu Ala Gln Ala Trp Phe Asn Thr His Arg Glu Leu Leu Glu
                165                 170                 175
Ser Asn Phe Thr Leu Val Gly Asp Asp Gly Thr Asn Lys Glu Ala Thr
            180                 185                 190
Ser Thr Gly Lys Leu Asn Gln Glu Asn Glu His Ile Tyr Asn Leu Trp
```



```
        195                 200                 205
Cys Ser Gly Arg Val Cys Cys Glu Gly Met Leu Ile Gln Leu Arg Phe
    210                 215                 220
Leu Lys Arg Gln Asp Leu Leu Asn Val Leu Ala Arg Met Met Arg Pro
225                 230                 235                 240
Val Ser Asp Gln Val Gln Ile Lys Val Thr Met Asn Asp Glu Asp Met
                245                 250                 255
Asp Thr Tyr Val Phe Ala Val Gly Thr Arg Lys Ala Leu Val Arg Leu
            260                 265                 270
Gln Lys Glu Met Gln Asp Leu Ser Glu Phe Cys Ser Asp Lys Pro Lys
        275                 280                 285
Ser Gly Ala Lys Tyr Gly Leu Pro Asp Ser Leu Ala Ile Leu Ser Glu
    290                 295                 300
Met Gly Glu Val Thr Asp Gly Met Met Asp Thr Lys Met Val His Phe
305                 310                 315                 320
Leu Thr His Tyr Ala Asp Lys Ile Glu Ser Val His Phe Ser Asp Gln
                325                 330                 335
Phe Ser Gly Pro Lys Ile Met Gln Glu Glu Gly Gln Pro Leu Lys Leu
            340                 345                 350
Pro Asp Thr Lys Arg Thr Leu Leu Phe Thr Phe Asn Val Pro Gly Ser
        355                 360                 365
Gly Asn Thr Tyr Pro Lys Asp Met Glu Ala Leu Leu Pro Leu Met Asn
    370                 375                 380
Met Val Ile Tyr Ser Ile Asp Lys Ala Lys Lys Phe Arg Leu Asn Arg
385                 390                 395                 400
Glu Gly Lys Gln Lys Ala Asp Lys Asn Arg Ala Arg Val Glu Glu Asn
                405                 410                 415
Phe Leu Lys Leu Thr His Val Gln Arg Gln Glu Ala Ala Gln Ser Arg
            420                 425                 430
Arg Glu Glu Lys Lys Arg Ala Glu Lys Glu Arg Ile Met Asn Glu Glu
        435                 440                 445
Asp Pro Glu Lys Gln Arg Arg Leu Glu Glu Ala Ala Leu Arg Arg Glu
    450                 455                 460
Gln Lys Lys Leu Glu Lys Lys Gln Met Lys Met Lys Gln Ile Lys Val
465                 470                 475                 480
```

Lys Ala Met

<210> 122
<211> 334
<212> PRT
<213> Homo sapience

<400> 122
Met Val Glu Phe Ala Pro Leu Phe Met Pro Trp Glu Arg Arg Leu Gln
1 5 10 15
Thr Leu Ala Val Leu Gln Phe Val Phe Ser Phe Leu Ala Leu Ala Glu
20 25 30
Ile Cys Thr Val Gly Phe Ile Ala Leu Leu Phe Thr Arg Phe Trp Leu
35 40 45
Leu Thr Val Leu Tyr Ala Ala Trp Trp Tyr Leu Asp Arg Asp Lys Pro
50 55 60
Arg Gln Gly Gly Arg His Ile Gln Ala Ile Arg Cys Trp Thr Ile Trp
65 70 75 80
Lys Tyr Met Lys Asp Tyr Phe Pro Ile Ser Leu Val Lys Thr Ala Glu
85 90 95
Leu Asp Pro Ser Arg Asn Tyr Ile Ala Gly Phe His Pro His Gly Val
100 105 110
Leu Ala Val Gly Ala Phe Ala Asn Leu Cys Thr Glu Ser Thr Gly Phe
115 120 125
Ser Ser Ile Phe Pro Gly Ile Arg Pro His Leu Met Met Leu Thr Leu
130 135 140
Trp Phe Arg Ala Pro Phe Phe Arg Asp Tyr Ile Met Ser Ala Gly Leu
145 150 155 160
Val Thr Ser Glu Lys Glu Ser Ala Ala His Ile Leu Asn Arg Lys Gly
165 170 175
Gly Gly Asn Leu Leu Gly Ile Ile Val Gly Gly Ala Gln Glu Ala Leu
180 185 190
Asp Ala Arg Pro Gly Ser Phe Thr Leu Leu Leu Arg Asn Arg Lys Gly
195 200 205
Phe Val Arg Leu Ala Leu Thr His Gly Ala Pro Leu Val Pro Ile Phe

210 215 220
Ser Phe Gly Glu Asn Asp Leu Phe Asp Gln Ile Pro Asn Ser Ser Gly
225 230 235 240
Ser Trp Leu Arg Tyr Ile Gln Asn Arg Leu Gln Lys Ile Met Gly Ile
245 250 255
Ser Leu Pro Leu Phe His Gly Arg Gly Val Phe Gln Tyr Ser Phe Gly
260 265 270
Leu Ile Pro Tyr Arg Arg Pro Ile Thr Thr Val Val Gly Lys Pro Ile
275 280 285
Glu Val Gln Lys Thr Leu His Pro Ser Glu Glu Glu Val Asn Gln Leu
290 295 300
His Gln Arg Tyr Ile Lys Glu Leu Cys Asn Leu Phe Glu Ala His Lys
305 310 315 320
Leu Lys Phe Asn Ile Pro Ala Asp Gln His Leu Glu Phe Cys
325 330

<210> 123
<211> 267
<212> PRT
<213> Homo sapience

<400> 123
Met Ala Pro Trp Ala Leu Leu Ser Pro Gly Val Leu Val Arg Thr Gly
1 5 10 15
His Thr Val Leu Thr Trp Gly Ile Thr Leu Val Leu Phe Leu His Asp
20 25 30
Thr Glu Leu Arg Gln Trp Glu Glu Gln Gly Glu Leu Leu Leu Pro Leu
35 40 45
Thr Phe Leu Leu Leu Val Leu Gly Ser Leu Leu Leu Tyr Leu Ala Val
50 55 60
Ser Leu Met Asp Pro Gly Tyr Val Asn Val Gln Pro Gln Pro Gln Glu
65 70 75 80
Glu Leu Lys Glu Glu Gln Thr Ala Met Val Pro Pro Ala Ile Pro Leu
85 90 95
Arg Arg Cys Arg Tyr Cys Leu Val Leu Gln Pro Leu Arg Ala Arg His

100 105 110
Cys Arg Glu Cys Arg Arg Cys Val Arg Arg Tyr Asp His His Cys Pro
115 120 125
Trp Met Glu Asn Cys Val Gly Glu Arg Asn His Pro Leu Phe Val Val
130 135 140
Tyr Leu Ala Leu Gln Leu Val Val Leu Leu Trp Gly Leu Tyr Leu Ala
145 150 155 160
Trp Ser Gly Leu Arg Phe Phe Gln Pro Trp Gly Leu Trp Leu Arg Ser
165 170 175
Ser Gly Leu Leu Phe Ala Thr Phe Leu Leu Leu Ser Leu Phe Ser Leu
180 185 190
Val Ala Ser Leu Leu Leu Val Ser His Leu Tyr Leu Val Ala Ser Asn
195 200 205
Thr Thr Thr Trp Glu Phe Ile Ser Ser His Arg Ile Ala Tyr Leu Arg
210 215 220
Gln Arg Pro Ser Asn Pro Phe Asp Arg Gly Leu Thr Arg Asn Leu Ala
225 230 235 240
His Phe Phe Cys Gly Trp Pro Ser Gly Ser Trp Glu Thr Leu Trp Ala
245 250 255
Glu Glu Glu Glu Glu Gly Ser Ser Pro Ala Val
260 265

<210> 124
<211> 106
<212> PRT
<213> Homo sapience

<400> 124
Met Ser Thr Asn Asn Met Ser Asp Pro Arg Arg Pro Asn Lys Val Leu
1 5 10 15
Arg Tyr Lys Pro Pro Pro Ser Glu Cys Asn Pro Ala Leu Asp Asp Pro
20 25 30
Thr Pro Asp Tyr Met Asn Leu Leu Gly Met Ile Phe Ser Met Cys Gly
35 40 45
Leu Met Leu Lys Leu Lys Trp Cys Ala Trp Val Ala Val Tyr Cys Ser

50 55 60
Phe Ile Ser Phe Ala Asn Ser Arg Ser Ser Glu Asp Thr Lys Gln Met
65 70 75 80
Met Ser Ser Phe Met Leu Ser Ile Ser Ala Val Val Met Ser Tyr Leu
85 90 95
Gln Asn Pro Gln Pro Met Thr Pro Pro Trp
100 105

<210> 125
<211> 224
<212> PRT
<213> Homo sapience

<400> 125
Met Thr Leu Phe His Phe Gly Asn Cys Phe Ala Leu Ala Tyr Phe Pro
1 5 10 15
Tyr Phe Ile Thr Tyr Lys Cys Ser Gly Leu Ser Glu Tyr Asn Ala Phe
20 25 30
Trp Lys Cys Val Gln Ala Gly Val Thr Tyr Leu Phe Val Gln Leu Cys
35 40 45
Lys Met Leu Phe Leu Ala Thr Phe Phe Pro Thr Trp Glu Gly Gly Ile
50 55 60
Tyr Asp Phe Ile Gly Glu Phe Met Lys Ala Ser Val Asp Val Ala Asp
65 70 75 80
Leu Ile Gly Leu Asn Leu Val Met Ser Arg Asn Ala Gly Lys Gly Glu
85 90 95
Tyr Lys Ile Met Val Ala Ala Leu Gly Trp Ala Thr Ala Glu Leu Ile
100 105 110
Met Ser Arg Cys Ile Pro Leu Trp Val Gly Ala Arg Gly Ile Glu Phe
115 120 125
Asp Trp Lys Tyr Ile Gln Met Ser Ile Asp Ser Asn Ile Ser Leu Val
130 135 140
His Tyr Ile Val Ala Ser Ala Gln Val Trp Met Ile Thr Arg Tyr Asp
145 150 155 160
Leu Tyr His Thr Phe Arg Pro Ala Val Leu Leu Leu Met Phe Leu Ser

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                165                 170                 175
Val Tyr Lys Ala Phe Val Met Glu Thr Phe Val His Leu Cys Ser Leu
            180                 185                 190
Gly Ser Trp Ala Ala Leu Leu Ala Arg Ala Val Val Thr Gly Leu Leu
        195                 200                 205
Ala Leu Ser Thr Leu Ala Leu Tyr Val Ala Val Val Asn Val His Ser
    210                 215                 220

<210> 126
<211> 258
<212> PRT
<213> Homo sapience

<400> 126
Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
  1               5                  10                  15
Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
             20                  25                  30
Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
         35                  40                  45
Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
     50                  55                  60
Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
 65                  70                  75                  80
Arg Arg Ser Met Phe Leu Met Thr Cys Lys Pro Pro Leu Tyr Met Gly
                 85                  90                  95
Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys Thr Ile Asp Glu Glu Leu
            100                 105                 110
Glu Arg Asp Lys Arg Val Thr Trp Ile Val Glu Phe Phe Ala Asn Trp
        115                 120                 125
Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile Tyr Ala Asp Leu Ser Leu
    130                 135                 140
Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly Lys Val Asp Val Gly Arg
145                 150                 155                 160
Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val Ser Thr Ser Pro Leu Thr
```



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                165                 170                 175
Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln Gly Gly Lys Glu Ala Met
            180                 185                 190
Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg Ala Val Ser Trp Thr Phe
        195                 200                 205
Ser Glu Glu Asn Val Ile Arg Glu Phe Asn Leu Asn Glu Leu Tyr Gln
    210                 215                 220
Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp Asn Ile Pro Glu Glu Gln
225                 230                 235                 240
Pro Val Ala Ser Thr Pro Thr Thr Val Ser Asp Gly Glu Asn Lys Lys
                245                 250                 255
Asp Lys

<210> 127
<211> 110
<212> PRT
<213> Homo sapience

<400> 127
Met Ala Ala Val Val Ala Lys Arg Glu Gly Pro Pro Phe Ile Ser Glu
  1               5                  10                  15
Ala Ala Val Arg Gly Asn Ala Ala Val Leu Asp Tyr Cys Arg Thr Ser
             20                  25                  30
Val Ser Ala Leu Ser Gly Ala Thr Ala Gly Ile Leu Gly Leu Thr Gly
         35                  40                  45
Leu Tyr Gly Phe Ile Phe Tyr Leu Leu Ala Ser Val Leu Leu Ser Leu
     50                  55                  60
Leu Leu Ile Leu Lys Ala Gly Arg Arg Trp Asn Lys Tyr Phe Lys Ser
 65                  70                  75                  80
Arg Arg Pro Leu Phe Thr Gly Gly Leu Ile Gly Gly Leu Phe Thr Tyr
                 85                  90                  95
Val Leu Phe Trp Thr Phe Leu Tyr Gly Met Val His Val Tyr
            100                 105                 110

<210> 128
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<211> 91
<212> PRT
<213> Homo sapience

<400> 128
Met Val Tyr Ile Ser Asn Gly Gln Val Leu Asp Ser Arg Ser Gln Ser
1 5 10 15
Pro Trp Arg Leu Ser Leu Ile Thr Asp Phe Phe Trp Gly Ile Ala Glu
20 25 30
Phe Val Val Leu Phe Phe Lys Thr Leu Leu Gln Gln Asp Val Lys Lys
35 40 45
Arg Arg Ser Tyr Gly Asn Ser Ser Asp Ser Arg Tyr Asp Asp Gly Arg
50 55 60
Gly Pro Pro Gly Asn Pro Pro Arg Arg Met Gly Arg Ile Asn His Leu
65 70 75 80
Arg Gly Pro Ser Pro Pro Pro Met Ala Gly Gly
85 90

<210> 129
<211> 344
<212> PRT
<213> Homo sapience

<400> 129
Met Phe Thr Ser Thr Gly Ser Ser Gly Leu Tyr Lys Ala Pro Leu Ser
1 5 10 15
Lys Ser Leu Leu Leu Val Pro Ser Ala Leu Ser Leu Leu Leu Ala Leu
20 25 30
Leu Leu Pro His Cys Gln Lys Leu Phe Val Tyr Asp Leu His Ala Val
35 40 45
Lys Asn Asp Phe Gln Ile Trp Arg Leu Ile Cys Gly Arg Ile Ile Cys
50 55 60
Leu Asp Leu Lys Asp Thr Phe Cys Ser Ser Leu Leu Ile Tyr Asn Phe
65 70 75 80
Arg Ile Phe Glu Arg Arg Tyr Gly Ser Arg Lys Phe Ala Ser Phe Leu

85 90 95
Leu Gly Ser Trp Val Leu Ser Ala Leu Phe Asp Phe Leu Leu Ile Glu
100 105 110
Ala Met Gln Tyr Phe Phe Gly Ile Thr Ala Ala Ser Asn Leu Pro Ser
115 120 125
Gly Phe Leu Ala Pro Val Phe Ala Leu Phe Val Pro Phe Tyr Cys Ser
130 135 140
Ile Pro Arg Val Gln Val Ala Gln Ile Leu Gly Pro Leu Ser Ile Thr
145 150 155 160
Asn Lys Thr Leu Ile Tyr Ile Leu Gly Leu Gln Leu Phe Thr Ser Gly
165 170 175
Ser Tyr Ile Trp Ile Val Ala Ile Ser Gly Leu Met Ser Gly Leu Cys
180 185 190
Tyr Asp Ser Lys Met Phe Gln Val His Gln Val Leu Cys Ile Pro Ser
195 200 205
Trp Met Ala Lys Phe Phe Ser Trp Thr Leu Glu Pro Ile Phe Ser Ser
210 215 220
Ser Glu Pro Thr Ser Glu Ala Arg Ile Gly Met Gly Ala Thr Leu Asp
225 230 235 240
Ile Gln Arg Gln Gln Arg Met Glu Leu Leu Asp Arg Gln Leu Met Phe
245 250 255
Ser Gln Phe Ala Gln Gly Arg Arg Gln Arg Gln Gln Gln Gly Gly Met
260 265 270
Ile Asn Trp Asn Arg Leu Phe Pro Pro Leu Arg Gln Arg Gln Asn Val
275 280 285
Asn Tyr Gln Gly Gly Arg Gln Ser Glu Pro Ala Ala Pro Pro Leu Glu
290 295 300
Val Ser Glu Glu Gln Val Ala Arg Leu Met Glu Met Gly Phe Ser Arg
305 310 315 320
Gly Asp Ala Leu Glu Ala Leu Arg Ala Ser Asn Asn Asp Leu Asn Val
325 330 335
Ala Thr Asn Phe Leu Leu Gln His
340

<210> 130

<211> 428

<212> PRT

<213> Homo sapience

<400> 130

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Met Gly Pro Pro Pro Gly Ala Gly Val Ser Cys Arg Gly Gly Cys Gly
1               5                   10                  15
Phe Ser Arg Leu Leu Ala Trp Cys Phe Leu Leu Ala Leu Ser Pro Gln
            20                  25                  30
Ala Pro Gly Ser Arg Gly Ala Glu Ala Val Trp Thr Ala Tyr Leu Asn
        35                  40                  45
Val Ser Trp Arg Val Pro His Thr Gly Val Asn Arg Thr Val Trp Glu
    50                  55                  60
Leu Ser Glu Glu Gly Val Tyr Gly Gln Asp Ser Pro Leu Glu Pro Val
65                  70                  75                  80
Ala Gly Val Leu Val Pro Pro Asp Gly Pro Gly Ala Leu Asn Ala Cys
                85                  90                  95
Asn Pro His Thr Asn Phe Thr Val Pro Thr Val Trp Gly Ser Thr Val
            100                 105                 110
Gln Val Ser Trp Leu Ala Leu Ile Gln Arg Gly Gly Gly Cys Thr Phe
        115                 120                 125
Ala Asp Lys Ile His Leu Ala Tyr Glu Arg Gly Ala Ser Gly Ala Val
    130                 135                 140
Ile Phe Asn Phe Pro Gly Thr Arg Asn Glu Val Ile Pro Met Ser His
145                 150                 155                 160
Pro Gly Ala Val Asp Ile Val Ala Ile Met Ile Gly Asn Leu Lys Gly
                165                 170                 175
Thr Lys Ile Leu Gln Ser Ile Gln Arg Gly Ile Gln Val Thr Met Val
            180                 185                 190
Ile Glu Val Gly Lys Lys His Gly Pro Trp Val Asn His Tyr Ser Ile
        195                 200                 205
Phe Phe Val Ser Val Ser Phe Phe Ile Ile Thr Ala Ala Thr Val Gly
    210                 215                 220
Tyr Phe Ile Phe Tyr Ser Ala Arg Arg Leu Arg Asn Ala Arg Ala Gln
225                 230                 235                 240
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Ser Arg Lys Gln Arg Gln Leu Lys Ala Asp Ala Lys Lys Ala Ile Gly
                245                 250                 255
Arg Leu Gln Leu Arg Thr Leu Lys Gln Gly Asp Lys Glu Ile Gly Pro
            260                 265                 270
Asp Gly Asp Ser Cys Ala Val Cys Ile Glu Leu Tyr Lys Pro Asn Asp
        275                 280                 285
Leu Val Arg Ile Leu Thr Cys Asn His Ile Phe His Lys Thr Cys Val
    290                 295                 300
Asp Pro Trp Leu Leu Glu His Arg Thr Cys Pro Met Cys Lys Cys Asp
305                 310                 315                 320
Ile Leu Lys Ala Leu Gly Ile Glu Val Asp Val Glu Asp Gly Ser Val
                325                 330                 335
Ser Leu Gln Val Pro Val Ser Asn Glu Ile Ser Asn Ser Ala Ser Ser
            340                 345                 350
His Glu Glu Asp Asn Arg Ser Glu Thr Ala Ser Ser Gly Tyr Ala Ser
        355                 360                 365
Val Gln Gly Thr Asp Glu Pro Pro Leu Glu Glu His Val Gln Ser Thr
    370                 375                 380
Asn Glu Ser Leu Gln Leu Val Asn His Glu Ala Asn Ser Val Ala Val
385                 390                 395                 400
Asp Val Ile Pro His Val Asp Asn Pro Thr Phe Glu Glu Asp Glu Thr
                405                 410                 415
Pro Asn Gln Glu Thr Ala Val Arg Glu Ile Lys Ser
            420                 425
```

<210> 131

<211> 1449

<212> DNA

<213> Homo sapience

<400> 131

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atgaaagcct tccacacttt ctgtgttgtc cttctggtgt ttgggagtgt ctctgaagcc      60
aagtttgatg attttgagga tgaggaggac atagtagagt atgatgataa tgacttcgct     120
gaatttgagg atgtcatgga agactctgtt actgaatctc ctcaacgggt cataatcact     180
gaagatgatg aagatgagac cactgtggag ttggaagggc aggatgaaaa ccaagaagga     240
```

```
gattttgaag atgcagatac ccaggaggga gatactgaga gtgaaccata tgatgatgaa     300
gaatttgaag gttatgaaga caaaccagat acttcttcta gcaaaaataa agacccaata     360
acgattgttg atgttcctgc acacctccag aacagctggg agagttatta tctagaaatt     420
ttgatggtga ctggtctgct tgcttatatc atgaattaca tcattgggaa gaataaaaac     480
agtcgccttg cacaggcctg gtttaacact catagggagc ttttggagag caactttact     540
ttagtggggg atgatggaac taacaaagaa gccacaagca caggaaagtt gaaccaggag     600
aatgagcaca tctataacct gtggtgttct ggtcgagtgt gctgtgaggg catgcttatc     660
cagctgaggt tcctcaagag acaagactta ctgaatgtcc tggcccggat gatgaggcca     720
gtgagtgatc aagtgcaaat aaaagtaacc atgaatgatg aagacatgga tacctacgta     780
tttgctgttg gcacacggaa agccttggtg cgactacaga aagagatgca ggatttgagt     840
gagttttgta gtgataaacc taagtctgga gcaaagtatg gactgccgga ctctttggcc     900
atcctgtcag agatgggaga agtcacagac ggaatgatgg atacaaagat ggttcacttt     960
cttacacact atgctgacaa gattgaatct gttcattttt cagaccagtt ctctggtcca    1020
aaaattatgc aagaggaagg tcagccttta aagctacctg acactaagag gacactgttg    1080
tttacattta atgtgcctgg ctcaggtaac acttacccaa aggatatgga ggcactgcta    1140
cccctgatga acatggtgat ttattctatt gataaagcca aaaagttccg actcaacaga    1200
gaaggcaaac aaaaagcaga taagaaccgt gcccgagtag aagagaactt cttgaaactg    1260
acacatgtgc aaagacagga agcagcacag tctcggcggg aggagaaaaa aagagcagag    1320
aaggagcgaa tcatgaatga ggaagatcct gagaaacagc gcaggctgga ggaggctgca    1380
ttgaggcgtg agcaaaagaa gttggaaaag aagcaaatga aaatgaaaca aatcaaagtg    1440
aaagccatg                                                            1449
```

<210> 132
<211> 1002
<212> DNA
<213> Homo sapience

<400> 132

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atggtagagt tcgcgccctt gtttatgccg tgggagcgca ggctgcagac acttgctgtc      60
ctacagtttg tcttctcctt cttggcactg gccgagatct gcactgtggg cttcatagcc     120
ctcctgttta caagattctg gctcctcact gtcctgtatg cggcctggtg gtatctggac     180
cgagacaagc cacggcaggg gggccggcac atccaggcca tcaggtgctg gactatatgg     240
aagtacatga aggactattt ccccatctcg ctggtcaaga ctgctgagct ggacccctct     300
cggaactaca ttgcgggctt ccacccccat ggagtcctgg cagtcggagc ctttgccaac     360
ctgtgcactg agagcacagg cttctcttcg atcttccccg gtatccgccc ccatctgatg     420
```



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atgctgacct tgtggttccg ggcccccttc ttcagagatt acatcatgtc tgcagggttg     480
gtcacatcag aaaaggagag tgctgctcac attctgaaca ggaagggtgg cggaaacttg     540
ctgggcatca ttgtaggggg tgcccaggag gccctggatg ccaggcctgg atccttcacg     600
ctgttactgc ggaaccgaaa gggcttcgtc aggctcgccc tgacacacgg ggcaccccctg    660
gtgccaatct tctccttcgg ggagaatgac ctatttgacc agattcccaa ctcttctggc     720
tcctggttac gctatatcca gaatcggttg cagaagatca tgggcatctc cctcccactc     780
tttcatggcc gtggtgtctt ccagtacagc tttggtttaa taccctaccg ccggcccatc     840
accactgtgg tggggaagcc catcgaggta cagaagacgc tgcatccctc ggaggaggag     900
gtgaaccagc tgcaccagcg ttatatcaaa gagctgtgca acctcttcga ggcccacaaa     960
cttaagttca acatccctgc tgaccagcac ttggagttct gc                       1002
```

<210> 133
<211> 801
<212> DNA
<213> Homo sapience

<400> 133

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atggcgccct gggcgctcct cagccctggg gtcctggtgc ggaccgggca caccgtgctg      60
acctggggaa tcacgctggt gctcttcctg cacgataccg agctgcggca atgggaggag     120
caggggggagc tgctcctgcc cctcaccttc ctgctcctgg tgctgggctc cctgctgctc    180
tacctcgctg tgtcactcat ggaccctggc tacgtgaatg tgcagcccca gcctcaggag     240
gagctcaaag aggagcagac agccatggtt cctccagcca tccctcttcg gcgctgcaga     300
tactgcctgg tgctgcagcc cctgagggct cggcactgcc gtgagtgccg ccgttgcgtc     360
cgccgctacg accaccactg cccctggatg gagaactgtg tgggagagcg caaccaccca     420
ctctttgtgg tctacctggc gctgcagctg gtggtgcttc tgtggggcct gtacctggca     480
tggtcaggcc tccggttctt ccagccctgg ggtctgtggt tgcggtccag cgggctcctg     540
ttcgccacct tcctgctgct gtccctcttc tcgttggtgg ccagcctgct cctcgtctcg     600
cacctctacc tggtggccag caacaccacc acctgggaat tcatctcctc acaccgcatc     660
gcctatctcc gccagcgccc cagcaacccc ttcgaccgag gcctgacccg caacctggcc     720
cacttcttct gtggatggcc ctcagggtcc tgggagaccc tctgggctga ggaggaggaa     780
gagggcagca gcccagctgt t                                               801
```

<210> 134
<211> 318
<212> DNA

<213> Homo sapience

<400> 134
atgtccacta acaatatgtc ggacccacgg aggccgaaca aagtgctgag gtacaagccc 60
ccgccgagcg aatgtaaccc ggccttggac gacccgacgc cggactacat gaacctgctg 120
ggcatgatct tcagcatgtg cggcctcatg cttaagctga agtggtgtgc ttgggtcgct 180
gtctactgct ccttcatcag ctttgccaac tctcggagct cggaggacac gaagcaaatg 240
atgagtagct tcatgctgtc catctctgcc gtggtgatgt cctatctgca gaatcctcag 300
cccatgacgc ccccatgg 318

<210> 135
<211> 672
<212> DNA
<213> Homo sapience

<400> 135
atgaccctgt ttcacttcgg gaactgcttc gctcttgcct acttccccta cttcatcacc 60
tacaagtgca gcggcctgtc cgagtacaac gccttctgga aatgcgtcca ggctggagtc 120
acctacctct ttgtccaact ctgcaagatg ctgttcttgg ccactttctt tcccacctgg 180
gaaggcggca tctatgactt cattggggag ttcatgaagg ccagcgtgga tgtggcagac 240
ctgataggtc taaaccttgt catgtcccgg aatgccggca agggagagta caagatcatg 300
gttgctgccc tgggctgggc cactgctgag cttattatgt cccgctgcat tcccctatgg 360
gtcggagccc ggggcattga gtttgactgg aagtacatcc agatgagcat agactccaac 420
atcagtctgg tccattacat cgtcgcgtct gctcaggtct ggatgataac acgctatgat 480
ctgtaccaca ccttccggcc agctgtcctc ctgctgatgt tcctcagtgt ctacaaggcc 540
tttgttatgg agaccttcgt ccacctctgc tcgctgggca gttgggcagc tctactggcc 600
cgagcagtgg taacggggct gctggccctc agcactttgg ccctgtatgt cgccgttgtc 660
aatgtgcact cc 672

<210> 136
<211> 774
<212> DNA
<213> Homo sapience

<400> 136

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ctcgcccaac cttactacct tctgtcggcc ctgctctctg ctgccttcct actcgtgagg 120
aaactgccgc cgctctgcca cggtctgccc acccaacgcg aagacggtaa cccgtgtgac 180
tttgactgga gagaagtgga gatcctgatg tttctcagtg ccattgtgat gatgaagaac 240
cgcagatcca tgttcctgat gacgtgcaaa cccccccctat atatgggccc tgagtatatc 300
aagtacttca atgataaaac cattgatgag gaactagaac gggacaagag ggtcacttgg 360
attgtggagt tctttgccaa ttggtctaat gactgccaat catttgcccc tatctatgct 420
gacctctccc ttaaatacaa ctgtacaggg ctaaattttg ggaaggtgga tgttggacgc 480
tatactgatg ttagtacgcg gtacaaagtg agcacatcac ccctcaccaa gcaactccct 540
accctgatcc tgttccaagg tggcaaggag gcaatgcggc ggccacagat tgacaagaaa 600
ggacgggctg tctcatggac cttctctgag gagaatgtga tccgagaatt taacttaaat 660
gagctatacc agcgggccaa gaaactatca aaggctggag acaatatccc tgaggagcag 720
cctgtggctt caacccccac cacagtgtca gatggggaaa acaagaagga taaa 774

<210> 137
<211> 330
<212> DNA
<213> Homo sapience

<400> 137
atggccgcgg tggtggccaa gcgggaaggg ccgccgttca tcagcgaggc ggccgtgcgg 60
ggcaacgccg ccgtcctgga ttattgccgg acctcggtgt cagcgctgtc gggggccacg 120
gccggcatcc tcggcctcac cggcctctac ggcttcatct tctacctgct cgcctccgtc 180
ctgctctccc tgctcctcat tctcaaggcg ggaaggaggt ggaacaaata tttcaaatca 240
cggagacctc tctttacagg aggcctcatc gggggcctct tcacctacgt cctgttctgg 300
acgttcctct acggcatggt gcacgtctac 330

<210> 138
<211> 273
<212> DNA
<213> Homo sapience

<400> 138
atggtttaca tctcgaacgg acaagtgttg gacagccgga gtcagtctcc atggagatta 60
tctttgataa cagatttctt ctggggaata gctgagtttg tggttttgtt tttcaaaact 120

ctgcttcagc aagatgtgaa aaaaagaaga agctatggaa actcatctga ttccagatat 180
gatgatggaa gagggccacc aggaaaccct ccccgaagaa tgggtagaat caatcatctg 240
cgtggcccta gtccccctcc aatggctggt gga 273

<210> 139
<211> 1032
<212> DNA
<213> Homo sapience

<400> 139
atgttcacca gcaccggctc cagtgggctc tacaaggcgc ctctgtcgaa gagccttctg 60
ctggtcccca gtgccctctc cctcctgctc gccctcctcc tgcctcactg ccagaagctc 120
tttgtgtatg accttcacgc agtcaagaac gacttccaga tttggaggtt gatatgtgga 180
agaataattt gccttgattt gaaagatact ttctgcagta gtctgcttat ttataatttt 240
aggatatttg aaagaagata tggaagcaga aaatttgcat cctttttgct gggttcctgg 300
gttttgtcag ccttatttga ctttctcctc attgaagcta tgcagtattt ctttggcatc 360
actgcagcta gtaatttgcc ttctggattc ctggcacctg tgtttgctct gtttgtacca 420
ttttactgct ccataccaag agtccaagtg gcacaaattc tgggtccgtt gtccatcaca 480
aacaagacat tgatttatat attgggactg cagcttttca cctctggttc ctacatctgg 540
attgtagcca taagtggact tatgtccggt ctgtgctacg acagcaaaat gttccaggtg 600
catcaggtgc tctgcatccc cagctggatg gcaaaattct ttctttggac acttgaaccc 660
atcttctctt cttcagaacc caccagcgaa gccagaattg ggatgggagc cacgctggac 720
atccagagac agcagagaat ggagctgctg gaccggcagc tgatgttctc tcagtttgca 780
caagggaggc gacagagaca gcagcaggga ggaatgatca attggaatcg tctttttcct 840
cctttacgtc agcgacaaaa cgtaaactat cagggcggtc ggcagtctga gccagcagcg 900
ccccctctag aagtttctga ggaacaggtc gcccggctca tggagatggg attttccaga 960
ggtgatgctt tggaagccct gagagcttca aacaatgacc tcaatgtcgc caccaacttc 1020
ctgctgcagc ac 1032

<210> 140
<211> 1284
<212> DNA
<213> Homo sapience

<400> 140

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ctggcatggt gcttcctgct ggccctgagt ccgcaggcac ccggttcccg gggggctgaa 120
gcagtgtgga ccgcgtacct caacgtgtcc tggcgggttc cgcacacggg agtgaaccgt 180
acggtgtggg agctgagcga ggagggcgtg tacggccagg actcgccgct ggagcctgtg 240
gctggggtcc tggtaccgcc cgacgggccc ggggcgctta acgcctgtaa cccgcacacg 300
aatttcacgg tgcccacggt ttggggaagc accgtgcaag tctcttggtt ggccctcatc 360
caacgcggcg ggggctgcac cttcgcagac aagatccatc tggcttatga gagaggggcg 420
tctggagccg tcatctttaa cttccccggg acccgcaatg aggtcatccc catgtctcac 480
ccgggtgcag tagacattgt tgcaatcatg atcggcaatc tgaaaggcac aaaaattctg 540
caatctattc aaagaggcat acaagtgaca atggtcatag aagtagggaa aaaacatggc 600
ccttgggtga atcactattc aattttttc gtttctgtgt cctttttat tattacggcg 660
gcaactgtgg gctattttat ctttattct gctcgaaggc tacggaatgc aagagctcaa 720
agcaggaagc agaggcaatt aaaggcagat gctaaaaaag ctattggaag gcttcaacta 780
cgcacactga aacaaggaga caaggaaatt ggccctgatg gagatagttg tgctgtgtgc 840
attgaattgt ataaaccaaa tgatttggta cgcatcttaa cgtgcaacca tattttccat 900
aagacatgtg ttgacccatg gctgttagaa cacaggactt gccccatgtg caaatgtgac 960
atactcaaag ctttgggaat tgaggtggat gttgaagatg gatcagtgtc tttacaagtc 1020
cctgtatcca atgaaatatc taatagtgcc tcctcccatg aagaggataa tcgcagcgag 1080
accgcatcat ctggatatgc ttcagtacag ggaacagatg aaccgcctct ggaggaacac 1140
gtgcagtcaa caaatgaaag tctacagctg gtaaaccatg aagcaaattc tgtggcagtg 1200
gatgttattc ctcatgttga caaccccaacc tttgaagaag acgaaactcc taatcaagag 1260
actgctgttc gagaaattaa atct 1284

<210> 141
<211> 2050
<212> DNA
<213> Homo sapience
<220>
<221> CDS
<222> (122)...(1573)

<400> 141
aaaaaaccgc tgcgatcgcg gaggcggcgg ccaggccgag aggcaggccg ggcaggggtg 60
tcggacgcag ggcgctgggc cgggtttcgg cttcggccac agcttttttt ctcaaggtgc 120
a atg aaa gcc ttc cac act ttc tgt gtt gtc ctt ctg gtg ttt ggg 166

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Met Lys Ala Phe His Thr Phe Cys Val Val Leu Leu Val Phe Gly
  1               5                  10                  15
agt gtc tct gaa gcc aag ttt gat gat ttt gag gat gag gag gac ata      214
Ser Val Ser Glu Ala Lys Phe Asp Asp Phe Glu Asp Glu Glu Asp Ile
                 20                  25                  30
gta gag tat gat gat aat gac ttc gct gaa ttt gag gat gtc atg gaa      262
Val Glu Tyr Asp Asp Asn Asp Phe Ala Glu Phe Glu Asp Val Met Glu
             35                  40                  45
gac tct gtt act gaa tct cct caa cgg gtc ata atc act gaa gat gat      310
Asp Ser Val Thr Glu Ser Pro Gln Arg Val Ile Ile Thr Glu Asp Asp
         50                  55                  60
gaa gat gag acc act gtg gag ttg gaa ggg cag gat gaa aac caa gaa      358
Glu Asp Glu Thr Thr Val Glu Leu Glu Gly Gln Asp Glu Asn Gln Glu
     65                  70                  75
gga gat ttt gaa gat gca gat acc cag gag gga gat act gag agt gaa      406
Gly Asp Phe Glu Asp Ala Asp Thr Gln Glu Gly Asp Thr Glu Ser Glu
 80                  85                  90                  95
cca tat gat gat gaa gaa ttt gaa ggt tat gaa gac aaa cca gat act      454
Pro Tyr Asp Asp Glu Glu Phe Glu Gly Tyr Glu Asp Lys Pro Asp Thr
                100                 105                 110
tct tct agc aaa aat aaa gac cca ata acg att gtt gat gtt cct gca      502
Ser Ser Ser Lys Asn Lys Asp Pro Ile Thr Ile Val Asp Val Pro Ala
            115                 120                 125
cac ctc cag aac agc tgg gag agt tat tat cta gaa att ttg atg gtg      550
His Leu Gln Asn Ser Trp Glu Ser Tyr Tyr Leu Glu Ile Leu Met Val
        130                 135                 140
act ggt ctg ctt gct tat atc atg aat tac atc att ggg aag aat aaa      598
Thr Gly Leu Leu Ala Tyr Ile Met Asn Tyr Ile Ile Gly Lys Asn Lys
    145                 150                 155
aac agt cgc ctt gca cag gcc tgg ttt aac act cat agg gag ctt ttg      646
Asn Ser Arg Leu Ala Gln Ala Trp Phe Asn Thr His Arg Glu Leu Leu
160                 165                 170                 175
gag agc aac ttt act tta gtg ggg gat gat gga act aac aaa gaa gcc      694
Glu Ser Asn Phe Thr Leu Val Gly Asp Asp Gly Thr Asn Lys Glu Ala
                180                 185                 190
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aca agc aca gga aag ttg aac cag gag aat gag cac atc tat aac ctg      742
Thr Ser Thr Gly Lys Leu Asn Gln Glu Asn Glu His Ile Tyr Asn Leu
            195                 200                 205
tgg tgt tct ggt cga gtg tgc tgt gag ggc atg ctt atc cag ctg agg      790
Trp Cys Ser Gly Arg Val Cys Cys Glu Gly Met Leu Ile Gln Leu Arg
        210                 215                 220
ttc ctc aag aga caa gac tta ctg aat gtc ctg gcc cgg atg atg agg      838
Phe Leu Lys Arg Gln Asp Leu Leu Asn Val Leu Ala Arg Met Met Arg
    225                 230                 235
cca gtg agt gat caa gtg caa ata aaa gta acc atg aat gat gaa gac      886
Pro Val Ser Asp Gln Val Gln Ile Lys Val Thr Met Asn Asp Glu Asp
240                 245                 250                 255
atg gat acc tac gta ttt gct gtt ggc aca cgg aaa gcc ttg gtg cga      934
Met Asp Thr Tyr Val Phe Ala Val Gly Thr Arg Lys Ala Leu Val Arg
                260                 265                 270
cta cag aaa gag atg cag gat ttg agt gag ttt tgt agt gat aaa cct      982
Leu Gln Lys Glu Met Gln Asp Leu Ser Glu Phe Cys Ser Asp Lys Pro
            275                 280                 285
aag tct gga gca aag tat gga ctg ccg gac tct ttg gcc atc ctg tca     1030
Lys Ser Gly Ala Lys Tyr Gly Leu Pro Asp Ser Leu Ala Ile Leu Ser
        290                 295                 300
gag atg gga gaa gtc aca gac gga atg atg gat aca aag atg gtt cac     1078
Glu Met Gly Glu Val Thr Asp Gly Met Met Asp Thr Lys Met Val His
    305                 310                 315
ttt ctt aca cac tat gct gac aag att gaa tct gtt cat ttt tca gac     1126
Phe Leu Thr His Tyr Ala Asp Lys Ile Glu Ser Val His Phe Ser Asp
320                 325                 330                 335
cag ttc tct ggt cca aaa att atg caa gag gaa ggt cag cct tta aag     1174
Gln Phe Ser Gly Pro Lys Ile Met Gln Glu Glu Gly Gln Pro Leu Lys
                340                 345                 350
cta cct gac act aag agg aca ctg ttg ttt aca ttt aat gtg cct ggc     1222
Leu Pro Asp Thr Lys Arg Thr Leu Leu Phe Thr Phe Asn Val Pro Gly
            355                 360                 365
tca ggt aac act tac cca aag gat atg gag gca ctg cta ccc ctg atg     1270
Ser Gly Asn Thr Tyr Pro Lys Asp Met Glu Ala Leu Leu Pro Leu Met
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370 375 380
aac atg gtg att tat tct att gat aaa gcc aaa aag ttc cga ctc aac 1318
Asn Met Val Ile Tyr Ser Ile Asp Lys Ala Lys Lys Phe Arg Leu Asn
385 390 395
aga gaa ggc aaa caa aaa gca gat aag aac cgt gcc cga gta gaa gag 1366
Arg Glu Gly Lys Gln Lys Ala Asp Lys Asn Arg Ala Arg Val Glu Glu
400 405 410 415
aac ttc ttg aaa ctg aca cat gtg caa aga cag gaa gca gca cag tct 1414
Asn Phe Leu Lys Leu Thr His Val Gln Arg Gln Glu Ala Ala Gln Ser
420 425 430
cgg cgg gag gag aaa aaa aga gca gag aag gag cga atc atg aat gag 1462
Arg Arg Glu Glu Lys Lys Arg Ala Glu Lys Glu Arg Ile Met Asn Glu
435 440 445
gaa gat cct gag aaa cag cgc agg ctg gag gag gct gca ttg agg cgt 1510
Glu Asp Pro Glu Lys Gln Arg Arg Leu Glu Glu Ala Ala Leu Arg Arg
450 455 460
gag caa aag aag ttg gaa aag aag caa atg aaa atg aaa caa atc aaa 1558
Glu Gln Lys Lys Leu Glu Lys Lys Gln Met Lys Met Lys Gln Ile Lys
465 470 475
gtg aaa gcc atg taaagccatc ccagagattt gagttctgat gccacctgta 1610
Val Lys Ala Met
480
agctctgaat tcacaggaaa catgaaaaac gccagtccat ttctcaacct taaatttcag 1670
acagtcttgg gcaactgaga aatccttatt tcatcatcta ctctgtttgg ggtttggggt 1730
tttacagaga ttgaagatac ctggaaaggg ctctgtttca agaatttttt tttccagata 1790
atcaaattat tttgattatt ttataaaagg aatgatctat gaaatctgtg taggttttaa 1850
atattttaaa aattataata caaatcatca gtgcttttag tacttcagtg tttaaagaaa 1910
taccatgaaa tttataggta gataaccaga ttgttgcttt ttgtttaaac caagcagttg 1970
aaatggctat aaagactgac tctaaaccaa gattctgcaa ataatgattg gaattgcaca 2030
ataaacattg cttgatgttt 2050

<210> 142
<211> 2746
<212> DNA
<213> Homo sapience

<220>
<221> CDS
<222> (70)...(1074)

<400> 142
aaaacctgtg ggtgcctcag accacagcag agctcacaga acctgcggga gccaggctga 60
cccgccagc atg gta gag ttc gcg ccc ttg ttt atg ccg tgg gag cgc 108
Met Val Glu Phe Ala Pro Leu Phe Met Pro Trp Glu Arg
1 5 10
agg ctg cag aca ctt gct gtc cta cag ttt gtc ttc tcc ttc ttg gca 156
Arg Leu Gln Thr Leu Ala Val Leu Gln Phe Val Phe Ser Phe Leu Ala
15 20 25
ctg gcc gag atc tgc act gtg ggc ttc ata gcc ctc ctg ttt aca aga 204
Leu Ala Glu Ile Cys Thr Val Gly Phe Ile Ala Leu Leu Phe Thr Arg
30 35 40 45
ttc tgg ctc ctc act gtc ctg tat gcg gcc tgg tgg tat ctg gac cga 252
Phe Trp Leu Leu Thr Val Leu Tyr Ala Ala Trp Trp Tyr Leu Asp Arg
50 55 60
gac aag cca cgg cag ggg ggc cgg cac atc cag gcc atc agg tgc tgg 300
Asp Lys Pro Arg Gln Gly Gly Arg His Ile Gln Ala Ile Arg Cys Trp
65 70 75
act ata tgg aag tac atg aag gac tat ttc ccc atc tcg ctg gtc aag 348
Thr Ile Trp Lys Tyr Met Lys Asp Tyr Phe Pro Ile Ser Leu Val Lys
80 85 90
act gct gag ctg gac ccc tct cgg aac tac att gcg ggc ttc cac ccc 396
Thr Ala Glu Leu Asp Pro Ser Arg Asn Tyr Ile Ala Gly Phe His Pro
95 100 105
cat gga gtc ctg gca gtc gga gcc ttt gcc aac ctg tgc act gag agc 444
His Gly Val Leu Ala Val Gly Ala Phe Ala Asn Leu Cys Thr Glu Ser
110 115 120 125
aca ggc ttc tct tcg atc ttc ccc ggt atc cgc ccc cat ctg atg atg 492
Thr Gly Phe Ser Ser Ile Phe Pro Gly Ile Arg Pro His Leu Met Met
130 135 140
ctg acc ttg tgg ttc cgg gcc ccc ttc ttc aga gat tac atc atg tct 540
Leu Thr Leu Trp Phe Arg Ala Pro Phe Phe Arg Asp Tyr Ile Met Ser

145 150 155
gca ggg ttg gtc aca tca gaa aag gag agt gct gct cac att ctg aac 588
Ala Gly Leu Val Thr Ser Glu Lys Glu Ser Ala Ala His Ile Leu Asn
160 165 170
agg aag ggt ggc gga aac ttg ctg ggc atc att gta ggg ggt gcc cag 636
Arg Lys Gly Gly Gly Asn Leu Leu Gly Ile Ile Val Gly Gly Ala Gln
175 180 185
gag gcc ctg gat gcc agg cct gga tcc ttc acg ctg tta ctg cgg aac 684
Glu Ala Leu Asp Ala Arg Pro Gly Ser Phe Thr Leu Leu Leu Arg Asn
190 195 200 205
cga aag ggc ttc gtc agg ctc gcc ctg aca cac ggg gca ccc ctg gtg 732
Arg Lys Gly Phe Val Arg Leu Ala Leu Thr His Gly Ala Pro Leu Val
210 215 220
cca atc ttc tcc ttc ggg gag aat gac cta ttt gac cag att ccc aac 780
Pro Ile Phe Ser Phe Gly Glu Asn Asp Leu Phe Asp Gln Ile Pro Asn
225 230 235
tct tct ggc tcc tgg tta cgc tat atc cag aat cgg ttg cag aag atc 828
Ser Ser Gly Ser Trp Leu Arg Tyr Ile Gln Asn Arg Leu Gln Lys Ile
240 245 250
atg ggc atc tcc ctc cca ctc ttt cat ggc cgt ggt gtc ttc cag tac 876
Met Gly Ile Ser Leu Pro Leu Phe His Gly Arg Gly Val Phe Gln Tyr
255 260 265
agc ttt ggt tta ata ccc tac cgc cgg ccc atc acc act gtg gtg ggg 924
Ser Phe Gly Leu Ile Pro Tyr Arg Arg Pro Ile Thr Thr Val Val Gly
270 275 280 285
aag ccc atc gag gta cag aag acg ctg cat ccc tcg gag gag gag gtg 972
Lys Pro Ile Glu Val Gln Lys Thr Leu His Pro Ser Glu Glu Glu Val
290 295 300
aac cag ctg cac cag cgt tat atc aaa gag ctg tgc aac ctc ttc gag 1020
Asn Gln Leu His Gln Arg Tyr Ile Lys Glu Leu Cys Asn Leu Phe Glu
305 310 315
gcc cac aaa ctt aag ttc aac atc cct gct gac cag cac ttg gag ttc 1068
Ala His Lys Leu Lys Phe Asn Ile Pro Ala Asp Gln His Leu Glu Phe
320 325 330
tgc tgagcccaa agggcagggc caacattagg gagcccagca ggaggtgctg 1120

Cys
tgctgagaag acttcctgga ggtgtttgtt gaacatatct gcagagcctt cccagactcc 1180
tgcaaatcca acccatatca ggctgtaagt cagagcaggc aatgcagaag aggagaccag 1240
accaaggggt cagctggggc taggacagtg agggctgcta gaggggctgg gcctctcttt 1300
gcacatggac actgggcccc tctctatatt gagtggtctg ttaacattca ttggtggctg 1360
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gcatctcttc tactgcattc tgttggtcga agcaagtcac aacccagcag attcaaggag 1480
taaggaatag gatccccctc tggatgggag gagcagcaat gtcatattac aaaagggtgt 1540
ggacacatgc agggattctt actgccgtct ttgcaaacaa tccaccaaaa cttaaaaact 1600
aaaagcctga agcacaagca ctctccaccc caggcacaca caccctggaa ttccctgtgt 1660
gaccatggta ccaccactgt gtgtcccgag gatcccagct cagctttgca tcgctgccct 1720
atctccctct cgctctcccc tgttgatccc tcatgcacag ccacagcgag ctgtctaaaa 1780
cacaaagctg accgcgccat ttcctactca gcatccttcc atgaccctcc attgctccta 1840
ggatagggtt tggaccagtc tgaatccaga ggatcaggat ccagcaggaa ccagaggata 1900
atttgaggag ggtttaaaaa ggaaccattt tttgaggtgt gtgcactgtt tccaccctga 1960
ggcctggaag gatgaatgga agcagcagtt cctgaaccag gaagactcat gtgtgggggc 2020
cattgctggt caaggggcac gaacaggtct ggtgaccctg caagggagga gccaggagca 2080
agcattccca cttcaccttc ctccattcag tctgctgcca agttccccac tgcctgagcc 2140
caactagaag ctggagggaa ggagggcctg tggctgcagt ccaggcatgt aggcctcctg 2200
ggaaagggag aatggcaaag acaggcagag tggatctgga ggggtcaacg gaagacggaa 2260
catgtccact tccaggcccg agcttctcag cctgccgttt gccactctcc agcatctggc 2320
ccagcctgtc catcctcatc tctcttcctc ccttactccg tgctcccatc actcggaacc 2380
atttgcattt ctttgtctca gctatattgt ctcacctctg agtttttgcc catgatgttg 2440
gatgccatgg aatgccatat cctccccatt atctccccct tgtctggata attcctactc 2500
atcctacaat actgatttta tctgtgcaaa gaagtcttcc ccagtgcctc tggttgacag 2560
gggtttcctc tggcttctcc agactttctg ttcctccacc acagccctta gcaccctggg 2620
gaggaggtgt tgctgtccag gtaaatgctg cgccaatgcc cctgcctcta gtgcactccc 2680
tccagcctac ccacaaacag gacctgcatc ctgtctcaca aataaaactg aactcttgaa 2740
atggtg 2746

<210> 143
<211> 1136
<212> DNA
<213> Homo sapience
<220>

<221> CDS
<222> (32)...(835)

<400> 143
attcttccgg gtggggcccc gggccgaggc g atg gcg ccc tgg gcg ctc ctc 52
Met Ala Pro Trp Ala Leu Leu
1 5
agc cct ggg gtc ctg gtg cgg acc ggg cac acc gtg ctg acc tgg gga 100
Ser Pro Gly Val Leu Val Arg Thr Gly His Thr Val Leu Thr Trp Gly
10 15 20
atc acg ctg gtg ctc ttc ctg cac gat acc gag ctg cgg caa tgg gag 148
Ile Thr Leu Val Leu Phe Leu His Asp Thr Glu Leu Arg Gln Trp Glu
25 30 35
gag cag ggg gag ctg ctc ctg ccc ctc acc ttc ctg ctc ctg gtg ctg 196
Glu Gln Gly Glu Leu Leu Leu Pro Leu Thr Phe Leu Leu Leu Val Leu
40 45 50 55
ggc tcc ctg ctg ctc tac ctc gct gtg tca ctc atg gac cct ggc tac 244
Gly Ser Leu Leu Leu Tyr Leu Ala Val Ser Leu Met Asp Pro Gly Tyr
60 65 70
gtg aat gtg cag ccc cag cct cag gag gag ctc aaa gag gag cag aca 292
Val Asn Val Gln Pro Gln Pro Gln Glu Glu Leu Lys Glu Glu Gln Thr
75 80 85
gcc atg gtt cct cca gcc atc cct ctt cgg cgc tgc aga tac tgc ctg 340
Ala Met Val Pro Pro Ala Ile Pro Leu Arg Arg Cys Arg Tyr Cys Leu
90 95 100
gtg ctg cag ccc ctg agg gct cgg cac tgc cgt gag tgc cgc cgt tgc 388
Val Leu Gln Pro Leu Arg Ala Arg His Cys Arg Glu Cys Arg Arg Cys
105 110 115
gtc cgc cgc tac gac cac cac tgc ccc tgg atg gag aac tgt gtg gga 436
Val Arg Arg Tyr Asp His His Cys Pro Trp Met Glu Asn Cys Val Gly
120 125 130 135
gag cgc aac cac cca ctc ttt gtg gtc tac ctg gcg ctg cag ctg gtg 484
Glu Arg Asn His Pro Leu Phe Val Val Tyr Leu Ala Leu Gln Leu Val
140 145 150
gtg ctt ctg tgg ggc ctg tac ctg gca tgg tca ggc ctc cgg ttc ttc 532

Val Leu Leu Trp Gly Leu Tyr Leu Ala Trp Ser Gly Leu Arg Phe Phe
155 160 165
cag ccc tgg ggt ctg tgg ttg cgg tcc agc ggg ctc ctg ttc gcc acc 580
Gln Pro Trp Gly Leu Trp Leu Arg Ser Ser Gly Leu Leu Phe Ala Thr
170 175 180
ttc ctg ctg ctg tcc ctc ttc tcg ttg gtg gcc agc ctg ctc ctc gtc 628
Phe Leu Leu Leu Ser Leu Phe Ser Leu Val Ala Ser Leu Leu Leu Val
185 190 195
tcg cac ctc tac ctg gtg gcc agc aac acc acc acc tgg gaa ttc atc 676
Ser His Leu Tyr Leu Val Ala Ser Asn Thr Thr Thr Trp Glu Phe Ile
200 205 210 215
tcc tca cac cgc atc gcc tat ctc cgc cag cgc ccc agc aac ccc ttc 724
Ser Ser His Arg Ile Ala Tyr Leu Arg Gln Arg Pro Ser Asn Pro Phe
220 225 230
gac cga ggc ctg acc cgc aac ctg gcc cac ttc ttc tgt gga tgg ccc 772
Asp Arg Gly Leu Thr Arg Asn Leu Ala His Phe Phe Cys Gly Trp Pro
235 240 245
tca ggg tcc tgg gag acc ctc tgg gct gag gag gag gaa gag ggc agc 820
Ser Gly Ser Trp Glu Thr Leu Trp Ala Glu Glu Glu Glu Glu Gly Ser
250 255 260
agc cca gct gtt tagggttgct ggaggccggg ctaccgtctt gtgcctga 870
Ser Pro Ala Val
265
aaaccacggg gcctgtcccc agctggggtg agcgctcaga gggcctgggg ccctcactcc 930
tgcccacgcc tcccagaccc cagaacggag cttcaagtca gacagatccc tgccttggtg 990
ggcagttctg ccttccaagg aagaagggga agaaaaggac ctgtggtgg ctcaggccca 1050
agcagacccc gggctccacc ccagccccgc ccaggctgct gccagtgcac actttacaa 1110
atttaatata aagcaagtcc agtctt 1136

<210> 144
<211> 619
<212> DNA
<213> Homo sapience
<220>
<221> CDS

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<222> (13)...(333)

<400> 144
cttcgactcg ct atg tcc act aac aat atg tcg gac cca cgg agg ccg          48
              Met Ser Thr Asn Asn Met Ser Asp Pro Arg Arg Pro
                1               5                   10
aac aaa gtg ctg agg tac aag ccc ccg ccg agc gaa tgt aac ccg gcc       96
Asn Lys Val Leu Arg Tyr Lys Pro Pro Pro Ser Glu Cys Asn Pro Ala
        15                  20                  25
ttg gac gac ccg acg ccg gac tac atg aac ctg ctg ggc atg atc ttc      144
Leu Asp Asp Pro Thr Pro Asp Tyr Met Asn Leu Leu Gly Met Ile Phe
    30                  35                  40
agc atg tgc ggc ctc atg ctt aag ctg aag tgg tgt gct tgg gtc gct      192
Ser Met Cys Gly Leu Met Leu Lys Leu Lys Trp Cys Ala Trp Val Ala
45                  50                  55                  60
gtc tac tgc tcc ttc atc agc ttt gcc aac tct cgg agc tcg gag gac      240
Val Tyr Cys Ser Phe Ile Ser Phe Ala Asn Ser Arg Ser Ser Glu Asp
                65                  70                  75
acg aag caa atg atg agt agc ttc atg ctg tcc atc tct gcc gtg gtg      288
Thr Lys Gln Met Met Ser Ser Phe Met Leu Ser Ile Ser Ala Val Val
            80                  85                  90
atg tcc tat ctg cag aat cct cag ccc atg acg ccc cca tgg              340
Met Ser Tyr Leu Gln Asn Pro Gln Pro Met Thr Pro Pro Trp
        95                  100                 105
tgataccagc ctagaagggt cacatttgg acctgtcta tccactaggc ctgggctttg      390
gctgctaaac ctgctgcctt cagctgccat cctggacttc cctgaatgag gccgtctcgg    450
tgccccccagc tggatagagg gaacctggcc ctttcctagg gaacacccta ggcttacccc   510
tcctgcctcc cttcccctgc ctgctgctgg gggagatgct gtccatgttt ctaggggtat    570
tcatttgctt tctcgttgaa acctgttgtt aataaagttt ttcactcag                619

<210> 145
<211> 864
<212> DNA
<213> Homo sapience
<220>
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<221> CDS
<222> (111)...(785)

<400> 145
aggtgggtgc caggccctgg ccgtggcgaa agagccggcg gagccggaga cccgctcccg     60
gagacgccgc ctcgcgatcc ccgcgcgggc gggaccgggc ggccggcatc atg acc      116
                                                       Met Thr
                                                         1
ctg ttt cac ttc ggg aac tgc ttc gct ctt gcc tac ttc ccc tac ttc      164
Leu Phe His Phe Gly Asn Cys Phe Ala Leu Ala Tyr Phe Pro Tyr Phe
        5                   10                  15
atc acc tac aag tgc agc ggc ctg tcc gag tac aac gcc ttc tgg aaa      212
Ile Thr Tyr Lys Cys Ser Gly Leu Ser Glu Tyr Asn Ala Phe Trp Lys
    20                  25                  30
tgc gtc cag gct gga gtc acc tac ctc ttt gtc caa ctc tgc aag atg      260
Cys Val Gln Ala Gly Val Thr Tyr Leu Phe Val Gln Leu Cys Lys Met
35                  40                  45                  50
ctg ttc ttg gcc act ttc ttt ccc acc tgg gaa ggc ggc atc tat gac      308
Leu Phe Leu Ala Thr Phe Phe Pro Thr Trp Glu Gly Gly Ile Tyr Asp
                55                  60                  65
ttc att ggg gag ttc atg aag gcc agc gtg gat gtg gca gac ctg ata      356
Phe Ile Gly Glu Phe Met Lys Ala Ser Val Asp Val Ala Asp Leu Ile
            70                  75                  80
ggt cta aac ctt gtc atg tcc cgg aat gcc ggc aag gga gag tac aag      404
Gly Leu Asn Leu Val Met Ser Arg Asn Ala Gly Lys Gly Glu Tyr Lys
        85                  90                  95
atc atg gtt gct gcc ctg ggc tgg gcc act gct gag ctt att atg tcc      452
Ile Met Val Ala Ala Leu Gly Trp Ala Thr Ala Glu Leu Ile Met Ser
    100                 105                 110
cgc tgc att ccc cta tgg gtc gga gcc cgg ggc att gag ttt gac tgg      500
Arg Cys Ile Pro Leu Trp Val Gly Ala Arg Gly Ile Glu Phe Asp Trp
115                 120                 125                 130
aag tac atc cag atg agc ata gac tcc aac atc agt ctg gtc cat tac      548
Lys Tyr Ile Gln Met Ser Ile Asp Ser Asn Ile Ser Leu Val His Tyr
                135                 140                 145
```

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atc gtc gcg tct gct cag gtc tgg atg ata aca cgc tat gat ctg tac      596
Ile Val Ala Ser Ala Gln Val Trp Met Ile Thr Arg Tyr Asp Leu Tyr
            150                 155                 160
cac acc ttc cgg cca gct gtc ctc ctg ctg atg ttc ctc agt gtc tac      644
His Thr Phe Arg Pro Ala Val Leu Leu Leu Met Phe Leu Ser Val Tyr
        165                 170                 175
aag gcc ttt gtt atg gag acc ttc gtc cac ctc tgc tcg ctg ggc agt      692
Lys Ala Phe Val Met Glu Thr Phe Val His Leu Cys Ser Leu Gly Ser
    180                 185                 190
tgg gca gct cta ctg gcc cga gca gtg gta acg ggg ctg ctg gcc ctc      740
Trp Ala Ala Leu Leu Ala Arg Ala Val Val Thr Gly Leu Leu Ala Leu
195                 200                 205                 210
agc act ttg gcc ctg tat gtc gcc gtt gtc aat gtg cac tcc taggcttg     790
Ser Thr Leu Ala Leu Tyr Val Ala Val Val Asn Val His Ser
                215                 220
gtgtctcaga cattgatgta ccttttccct gcctcgctcc aggttttagt gaagtaaaca    850
gtatttggaa agtt                                                      864

<210> 146
<211> 1527
<212> DNA
<213> Homo sapience
<220>
<221> CDS
<222> (25)...(801)

<400> 146
gcagtggccg ttacggccga aaag atg gcg gtc ttg gca cct cta att gct       51
                           Met Ala Val Leu Ala Pro Leu Ile Ala
                             1               5
ctc gtg tat tcg gtg ccg cga ctt tca cga tgg ctc gcc caa cct tac      99
Leu Val Tyr Ser Val Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr
 10                  15                  20                  25
tac ctt ctg tcg gcc ctg ctc tct gct gcc ttc cta ctc gtg agg aaa      147
Tyr Leu Leu Ser Ala Leu Leu Ser Ala Ala Phe Leu Leu Val Arg Lys
```



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                 30                  35                  40
ctg ccg ccg ctc tgc cac ggt ctg ccc acc caa cgc gaa gac ggt aac      195
Leu Pro Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Asp Gly Asn
             45                  50                  55
ccg tgt gac ttt gac tgg aga gaa gtg gag atc ctg atg ttt ctc agt      243
Pro Cys Asp Phe Asp Trp Arg Glu Val Glu Ile Leu Met Phe Leu Ser
         60                  65                  70
gcc att gtg atg atg aag aac cgc aga tcc atg ttc ctg atg acg tgc      291
Ala Ile Val Met Met Lys Asn Arg Arg Ser Met Phe Leu Met Thr Cys
     75                  80                  85
aaa ccc ccc cta tat atg ggc cct gag tat atc aag tac ttc aat gat      339
Lys Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp
 90                  95                 100                 105
aaa acc att gat gag gaa cta gaa cgg gac aag agg gtc act tgg att      387
Lys Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile
                110                 115                 120
gtg gag ttc ttt gcc aat tgg tct aat gac tgc caa tca ttt gcc cct      435
Val Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro
            125                 130                 135
atc tat gct gac ctc tcc ctt aaa tac aac tgt aca ggg cta aat ttt      483
Ile Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe
        140                 145                 150
ggg aag gtg gat gtt gga cgc tat act gat gtt agt acg cgg tac aaa      531
Gly Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys
    155                 160                 165
gtg agc aca tca ccc ctc acc aag caa ctc cct acc ctg atc ctg ttc      579
Val Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe
170                 175                 180                 185
caa ggt ggc aag gag gca atg cgg cgg cca cag att gac aag aaa gga      627
Gln Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly
                190                 195                 200
cgg gct gtc tca tgg acc ttc tct gag gag aat gtg atc cga gaa ttt      675
Arg Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe
            205                 210                 215
aac tta aat gag cta tac cag cgg gcc aag aaa cta tca aag gct gga      723
```

```
Asn Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly
        220                 225                 230
gac aat atc cct gag gag cag cct gtg gct tca acc ccc acc aca gtg      771
Asp Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val
    235                 240                 245
tca gat ggg gaa aac aag aag gat aaa taagatcctc ac                    810
Ser Asp Gly Glu Asn Lys Lys Asp Lys
250                 255
tttggcagtg cttcctctcc tgtcaattcc aggctctttc cataaccaca agcctgaggc    870
tgcagccttt tatttatgtt ttccctttgg ctgtgactgg gtggggcagc atgcagcttc    930
tgattttaaa gaggcatcta gggaattgtc aggcaccctа caggaaggcc tgccatgctg    990
tggccaactg tttcactgga gcaagaaaga gatctcatag gacggagggg gaaatggttt   1050
ccctccaagc ttgggtcagt gtgttaactg cttatcagct attcagacat ctccatggtt   1110
tctccatgaa actctgtggt ttcatcattc cttcttagtt gacctgcaca gcttggttag   1170
acctagattt aaccctaagg taagatgctg ggtatagaa cgctaagaat tttcccccaa    1230
ggactcttgc ttccttaagc ccttctggct tcgtttatgg tcttcattaa aagtataagc   1290
ctaactttgt cgctagtcct aaggagaaac ctttaaccac aaagttttta tcattgaaga   1350
caatattgaa caacccccta ttttgtgggg attgagaagg ggtgaataga ggcttgagac   1410
tttcctttgt gtggtaggac ttggaggaga aatcccctgg actttcacta accctctgac   1470
atactcccca cacccagttg atggctttcc gtaataaaaa gattgggatt tcctttt      1527
```

<210> 147
<211> 659
<212> DNA
<213> Homo sapience
<220>
<221> CDS
<222> (138)...(470)

<400> 147

```
agtcttccga gcaagatggc gccgcgggca tttcttccac tgcccgtctg agggaacgct     60
aagtagtgtg tccggcgccg tgttccagct ccgcgttgtt ccgcgagaaa gcgagaggcc    120
gagcccgggc tggtgcg atg gcc gcg gtg gtg gcc aag cgg gaa ggg ccg       170
                   Met Ala Ala Val Val Ala Lys Arg Glu Gly Pro
                   1               5                   10
```



```
ccg ttc atc agc gag gcg gcc gtg cgg ggc aac gcc gcc gtc ctg gat      218
Pro Phe Ile Ser Glu Ala Ala Val Arg Gly Asn Ala Ala Val Leu Asp
            15                  20                  25
tat tgc cgg acc tcg gtg tca gcg ctg tcg ggg gcc acg gcc ggc atc      266
Tyr Cys Arg Thr Ser Val Ser Ala Leu Ser Gly Ala Thr Ala Gly Ile
        30                  35                  40
ctc ggc ctc acc ggc ctc tac ggc ttc atc ttc tac ctg ctc gcc tcc      314
Leu Gly Leu Thr Gly Leu Tyr Gly Phe Ile Phe Tyr Leu Leu Ala Ser
    45                  50                  55
gtc ctg ctc tcc ctg ctc ctc att ctc aag gcg gga agg agg tgg aac      362
Val Leu Leu Ser Leu Leu Leu Ile Leu Lys Ala Gly Arg Arg Trp Asn
60                  65                  70                  75
aaa tat ttc aaa tca cgg aga cct ctc ttt aca gga ggc ctc atc ggg      410
Lys Tyr Phe Lys Ser Arg Arg Pro Leu Phe Thr Gly Gly Leu Ile Gly
                80                  85                  90
ggc ctc ttc acc tac gtc ctg ttc tgg acg ttc ctc tac ggc atg gtg      458
Gly Leu Phe Thr Tyr Val Leu Phe Trp Thr Phe Leu Tyr Gly Met Val
            95                  100                 105
cac gtc tac tgaaatgggg gcccggggga ctttttaaa aaa                      500
His Val Tyr
        110
ccagatcggg aggactgtgg ccagcaatta acaccatgta gacttcctta gttcttaagt    560
ggttgaattc gctgcttgtt ctgtaacgtt ataaataatt tatatctgaa gacggagagc    620
ctgtaatatt cttcagatta aatgaagcgt gagacactt                           659
```

<210> 148
<211> 710
<212> DNA
<213> Homo sapience
<220>
<221> CDS
<222> (68)...(343)

<400> 148

```
agagggagat acagaaaccg acaggggcca ggcgcccggt ggctccgaag cggggaagtg     60
```

```
ggacaag atg gtt tac atc tcg aac gga caa gtg ttg gac agc cgg agt      109
        Met Val Tyr Ile Ser Asn Gly Gln Val Leu Asp Ser Arg Ser
          1               5                  10
cag tct cca tgg aga tta tct ttg ata aca gat ttc ttc tgg gga ata      157
Gln Ser Pro Trp Arg Leu Ser Leu Ile Thr Asp Phe Phe Trp Gly Ile
 15                  20                  25                  30
gct gag ttt gtg gtt ttg ttt ttc aaa act ctg ctt cag caa gat gtg      205
Ala Glu Phe Val Val Leu Phe Phe Lys Thr Leu Leu Gln Gln Asp Val
                 35                  40                  45
aaa aaa aga aga agc tat gga aac tca tct gat tcc aga tat gat gat      253
Lys Lys Arg Arg Ser Tyr Gly Asn Ser Ser Asp Ser Arg Tyr Asp Asp
             50                  55                  60
gga aga ggg cca cca gga aac cct ccc cga aga atg ggt aga atc aat      301
Gly Arg Gly Pro Pro Gly Asn Pro Pro Arg Arg Met Gly Arg Ile Asn
         65                  70                  75
cat ctg cgt ggc cct agt ccc cct cca atg gct ggt gga tgaggaaggt       350
His Leu Arg Gly Pro Ser Pro Pro Pro Met Ala Gly Gly
     80                  85                  90
aaatgtctgc tctaagaagc agacaaccgg acatgcgcat tcatagcaga aggaaaccat    410
caagaagtgg aaggctgacc atgatgagca gtagatgaat gtgtatgtct aaacaaggac    470
tgctctgtgt cctcacagat gaatgaggtc atgctgggaa ttccctctgc agggaactgg    530
cctgactgac atgcagttcc ataaatgcag atgtttgtct cattaccttt ttgtatagtt    590
tattaaagta ttaatatagt tttaataagt aaatattttt aggttgcaga atggactcct    650
catctttata ttcacgaaaa agcaatctga agaaaacaaa taaaagcctg tgtatttagc    710

<210> 149
<211> 2182
<212> DNA
<213> Homo sapience
<220>
<221> CDS
<222> (56)...(1090)

<400> 149
gcacttcagc ttcccctccc ccggcgccct ctggggctcc gagcccggcg ggacc          58
```



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atg ttc acc agc acc ggc tcc agt ggg ctc tac aag gcg cct ctg tcg      103
Met Phe Thr Ser Thr Gly Ser Ser Gly Leu Tyr Lys Ala Pro Leu Ser
  1               5                  10                  15
aag agc ctt ctg ctg gtc ccc agt gcc ctc tcc ctc ctg ctc gcc ctc      151
Lys Ser Leu Leu Leu Val Pro Ser Ala Leu Ser Leu Leu Leu Ala Leu
             20                  25                  30
ctc ctg cct cac tgc cag aag ctc ttt gtg tat gac ctt cac gca gtc      199
Leu Leu Pro His Cys Gln Lys Leu Phe Val Tyr Asp Leu His Ala Val
         35                  40                  45
aag aac gac ttc cag att tgg agg ttg ata tgt gga aga ata att tgc      247
Lys Asn Asp Phe Gln Ile Trp Arg Leu Ile Cys Gly Arg Ile Ile Cys
     50                  55                  60
ctt gat ttg aaa gat act ttc tgc agt agt ctg ctt att tat aat ttt      295
Leu Asp Leu Lys Asp Thr Phe Cys Ser Ser Leu Leu Ile Tyr Asn Phe
 65                  70                  75                  80
agg ata ttt gaa aga aga tat gga agc aga aaa ttt gca tcc ttt ttg      343
Arg Ile Phe Glu Arg Arg Tyr Gly Ser Arg Lys Phe Ala Ser Phe Leu
                 85                  90                  95
ctg ggt tcc tgg gtt ttg tca gcc tta ttt gac ttt ctc ctc att gaa      391
Leu Gly Ser Trp Val Leu Ser Ala Leu Phe Asp Phe Leu Leu Ile Glu
            100                 105                 110
gct atg cag tat ttc ttt ggc atc act gca gct agt aat ttg cct tct      439
Ala Met Gln Tyr Phe Phe Gly Ile Thr Ala Ala Ser Asn Leu Pro Ser
        115                 120                 125
gga ttc ctg gca cct gtg ttt gct ctg ttt gta cca ttt tac tgc tcc      487
Gly Phe Leu Ala Pro Val Phe Ala Leu Phe Val Pro Phe Tyr Cys Ser
    130                 135                 140
ata cca aga gtc caa gtg gca caa att ctg ggt ccg ttg tcc atc aca      535
Ile Pro Arg Val Gln Val Ala Gln Ile Leu Gly Pro Leu Ser Ile Thr
145                 150                 155                 160
aac aag aca ttg att tat ata ttg gga ctg cag ctt ttc acc tct ggt      583
Asn Lys Thr Leu Ile Tyr Ile Leu Gly Leu Gln Leu Phe Thr Ser Gly
                165                 170                 175
tcc tac atc tgg att gta gcc ata agt gga ctt atg tcc ggt ctg tgc      631
Ser Tyr Ile Trp Ile Val Ala Ile Ser Gly Leu Met Ser Gly Leu Cys
```

```
        180                 185                 190
tac gac agc aaa atg ttc cag gtg cat cag gtg ctc tgc atc ccc agc      679
Tyr Asp Ser Lys Met Phe Gln Val His Gln Val Leu Cys Ile Pro Ser
    195                 200                 205
tgg atg gca aaa ttc ttt tct tgg aca ctt gaa ccc atc ttc tct tct      727
Trp Met Ala Lys Phe Phe Ser Trp Thr Leu Glu Pro Ile Phe Ser Ser
210                 215                 220
tca gaa ccc acc agc gaa gcc aga att ggg atg gga gcc acg ctg gac      775
Ser Glu Pro Thr Ser Glu Ala Arg Ile Gly Met Gly Ala Thr Leu Asp
225                 230                 235                 240
atc cag aga cag cag aga atg gag ctg ctg gac cgg cag ctg atg ttc      823
Ile Gln Arg Gln Gln Arg Met Glu Leu Leu Asp Arg Gln Leu Met Phe
                245                 250                 255
tct cag ttt gca caa ggg agg cga cag aga cag cag cag gga gga atg      871
Ser Gln Phe Ala Gln Gly Arg Arg Gln Arg Gln Gln Gln Gly Gly Met
            260                 265                 270
atc aat tgg aat cgt ctt ttt cct cct tta cgt cag cga caa aac gta      919
Ile Asn Trp Asn Arg Leu Phe Pro Pro Leu Arg Gln Arg Gln Asn Val
        275                 280                 285
aac tat cag ggc ggt cgg cag tct gag cca gca gcg ccc cct cta gaa      967
Asn Tyr Gln Gly Gly Arg Gln Ser Glu Pro Ala Ala Pro Pro Leu Glu
    290                 295                 300
gtt tct gag gaa cag gtc gcc cgg ctc atg gag atg gga ttt tcc aga      1015
Val Ser Glu Glu Gln Val Ala Arg Leu Met Glu Met Gly Phe Ser Arg
305                 310                 315                 320
ggt gat gct ttg gaa gcc ctg aga gct tca aac aat gac ctc aat gtc      1063
Gly Asp Ala Leu Glu Ala Leu Arg Ala Ser Asn Asn Asp Leu Asn Val
                325                 330                 335
gcc acc aac ttc ctg ctg cag cac tgatagtccc aggccaacac tgg            1110
Ala Thr Asn Phe Leu Leu Gln His
            340
gaccggaccg gcagccgagt gacagtgcgt ggtccccacc atcagatcag cccggggacc    1170
gagcatctct ggtgctgatg ttcttgtggg aagagggagg ttccaccgca cccctgccct    1230
caaccgcaag actgttgccg ttttagtgtg gagataagtt tgccattaca ttagcatgta    1290
ttttctatct atatttttta ttgggcattt tccctaggtt ggagagtcag cactcgtttt    1350
```



```
gaatgtgttt aaaatgcatt aaaatggaag atttctgcag gcagttgaat ggcactccag    1410
atggggaatt gctgtaaccc tcttactgta acatgtcatc tcctgcgtcg tgatggggag    1470
agggtaatgt tacttcacaa aggacatgtc agatccttct tcatggactt ttttagttac    1530
tgtttttttct ctcaaacttg ttttcgaatc tcctgggagt gaggggagaaa cagggagctg  1590
aatcctcccc caagctgttc caggccagag gactctgcag taccttctcc tacatctagt    1650
aacaaagaat ggtgataacc atgcactggt tcaaggttct ggagttctcc atgaaacttg    1710
ggttaatttt gctcagagta tccggagtta gccactaggc tgcgggtgaa atgggatgga    1770
gtagaacaac agcaggcttc ctggagccac atgggctgac tagggcactc tgtggctggc    1830
ctggcacggg ctcagcccag gaagaggaga aacgatccct tgcctgcccc tccctgtggc    1890
agggctaact gcctggccct cctggctcgc agccagccag cccccctggca gcaggttctc   1950
ctcagggctt gggtcttcaa cctgtggcga caggaggcag ggcagactgt ggaggacagg    2010
atgcaggtca gggagaggga aggcaggggt ggaccgccat gagcatgaaa agacccgaag    2070
caagttgact cttgcaatgt gcaactgtta tgttctgcaa aatgagcaac gatgtatcaa    2130
attgatgcaa atttagatgt tgatacttac aataaagttt ttaatgtgtt tt            2182

<210> 150
<211> 2773
<212> DNA
<213> Homo sapience
<220>
<221> CDS
<222> (211)...(1497)

<400> 150
gtagcggaga agactggagc tccgaggagc tgcatctgcg gcaacctgtg tgctgacgct    60
acgtgcctcc tggctccgac gtagctcgca gctccccagt ctcactccat tccttcccca    120
cctggcgcgc acctgctcaa gaccagggtc ctgccaagcg ctaggagggc gcgtgccagg    180
ggcgctaggg aactgcggag cgcgcgcgcc atg ggg ccg ccg cct ggg gcc         231
                                 Met Gly Pro Pro Pro Gly Ala
                                   1               5
ggg gtc tcc tgc cgc ggt ggc tgc ggc ttt tcc aga ttg ctg gca tgg      279
Gly Val Ser Cys Arg Gly Gly Cys Gly Phe Ser Arg Leu Leu Ala Trp
        10                  15                  20
tgc ttc ctg ctg gcc ctg agt ccg cag gca ccc ggt tcc cgg ggg gct      327
Cys Phe Leu Leu Ala Leu Ser Pro Gln Ala Pro Gly Ser Arg Gly Ala
```

```
     25                   30                  35
gaa gca gtg tgg acc gcg tac ctc aac gtg tcc tgg cgg gtt ccg cac      375
Glu Ala Val Trp Thr Ala Tyr Leu Asn Val Ser Trp Arg Val Pro His
 40                  45                  50                  55
acg gga gtg aac cgt acg gtg tgg gag ctg agc gag gag ggc gtg tac      423
Thr Gly Val Asn Arg Thr Val Trp Glu Leu Ser Glu Glu Gly Val Tyr
                 60                  65                  70
ggc cag gac tcg ccg ctg gag cct gtg gct ggg gtc ctg gta ccg ccc      471
Gly Gln Asp Ser Pro Leu Glu Pro Val Ala Gly Val Leu Val Pro Pro
             75                  80                  85
gac ggg ccc ggg gcg ctt aac gcc tgt aac ccg cac acg aat ttc acg      519
Asp Gly Pro Gly Ala Leu Asn Ala Cys Asn Pro His Thr Asn Phe Thr
         90                  95                 100
gtg ccc acg gtt tgg gga agc acc gtg caa gtc tct tgg ttg gcc ctc      567
Val Pro Thr Val Trp Gly Ser Thr Val Gln Val Ser Trp Leu Ala Leu
    105                 110                 115
atc caa cgc ggc ggg ggc tgc acc ttc gca gac aag atc cat ctg gct      615
Ile Gln Arg Gly Gly Gly Cys Thr Phe Ala Asp Lys Ile His Leu Ala
120                 125                 130                 135
tat gag aga ggg gcg tct gga gcc gtc atc ttt aac ttc ccc ggg acc      663
Tyr Glu Arg Gly Ala Ser Gly Ala Val Ile Phe Asn Phe Pro Gly Thr
                140                 145                 150
cgc aat gag gtc atc ccc atg tct cac ccg ggt gca gta gac att gtt      711
Arg Asn Glu Val Ile Pro Met Ser His Pro Gly Ala Val Asp Ile Val
            155                 160                 165
gca atc atg atc ggc aat ctg aaa ggc aca aaa att ctg caa tct att      759
Ala Ile Met Ile Gly Asn Leu Lys Gly Thr Lys Ile Leu Gln Ser Ile
        170                 175                 180
caa aga ggc ata caa gtg aca atg gtc ata gaa gta ggg aaa aaa cat      807
Gln Arg Gly Ile Gln Val Thr Met Val Ile Glu Val Gly Lys Lys His
    185                 190                 195
ggc cct tgg gtg aat cac tat tca att ttt ttc gtt tct gtg tcc ttt      855
Gly Pro Trp Val Asn His Tyr Ser Ile Phe Phe Val Ser Val Ser Phe
200                 205                 210                 215
ttt att att acg gcg gca act gtg ggc tat ttt atc ttt tat tct gct      903
```



```
Phe Ile Ile Thr Ala Ala Thr Val Gly Tyr Phe Ile Phe Tyr Ser Ala
                220                 225                 230
cga agg cta cgg aat gca aga gct caa agc agg aag cag agg caa tta      951
Arg Arg Leu Arg Asn Ala Arg Ala Gln Ser Arg Lys Gln Arg Gln Leu
            235                 240                 245
aag gca gat gct aaa aaa gct att gga agg ctt caa cta cgc aca ctg      999
Lys Ala Asp Ala Lys Lys Ala Ile Gly Arg Leu Gln Leu Arg Thr Leu
        250                 255                 260
aaa caa gga gac aag gaa att ggc cct gat gga gat agt tgt gct gtg     1047
Lys Gln Gly Asp Lys Glu Ile Gly Pro Asp Gly Asp Ser Cys Ala Val
    265                 270                 275
tgc att gaa ttg tat aaa cca aat gat ttg gta cgc atc tta acg tgc     1095
Cys Ile Glu Leu Tyr Lys Pro Asn Asp Leu Val Arg Ile Leu Thr Cys
280                 285                 290                 295
aac cat att ttc cat aag aca tgt gtt gac cca tgg ctg tta gaa cac     1143
Asn His Ile Phe His Lys Thr Cys Val Asp Pro Trp Leu Leu Glu His
                300                 305                 310
agg act tgc ccc atg tgc aaa tgt gac ata ctc aaa gct ttg gga att     1191
Arg Thr Cys Pro Met Cys Lys Cys Asp Ile Leu Lys Ala Leu Gly Ile
            315                 320                 325
gag gtg gat gtt gaa gat gga tca gtg tct tta caa gtc cct gta tcc     1239
Glu Val Asp Val Glu Asp Gly Ser Val Ser Leu Gln Val Pro Val Ser
        330                 335                 340
aat gaa ata tct aat agt gcc tcc tcc cat gaa gag gat aat cgc agc     1287
Asn Glu Ile Ser Asn Ser Ala Ser Ser His Glu Glu Asp Asn Arg Ser
    345                 350                 355
gag acc gca tca tct gga tat gct tca gta cag gga aca gat gaa ccg     1335
Glu Thr Ala Ser Ser Gly Tyr Ala Ser Val Gln Gly Thr Asp Glu Pro
360                 365                 370                 375
cct ctg gag gaa cac gtg cag tca aca aat gaa agt cta cag ctg gta     1383
Pro Leu Glu Glu His Val Gln Ser Thr Asn Glu Ser Leu Gln Leu Val
                380                 385                 390
aac cat gaa gca aat tct gtg gca gtg gat gtt att cct cat gtt gac     1431
Asn His Glu Ala Asn Ser Val Ala Val Asp Val Ile Pro His Val Asp
            395                 400                 405
```

```
aac cca acc ttt gaa gaa gac gaa act cct aat caa gag act gct gtt     1479
Asn Pro Thr Phe Glu Glu Asp Glu Thr Pro Asn Gln Glu Thr Ala Val
        410                 415                 420
cga gaa att aaa tct taaaatctgt gtaaatagaa aacttgaacc attagt        1530
Arg Glu Ile Lys Ser
    425
aataacagaa ctgccaatca gggcctagtt tctattaata aattggataa atttaataaa  1590
ataagagtga tactgaaagt gctcagatga ctaatattat gctatagtta aatggcttaa  1650
aatatttaac ctgttaactt ttttccacaa actcattata atatttttca taggcaagtt  1710
tcctctcagt agtgataaca acatttttag acattcaaaa ctgtcttcaa gaagtcacgt  1770
ttttcattta taacaatttt cttataaaaa catgttgctt ttaaaatgtg gagtagctgt  1830
aatcacttta ttttatgata gtatcttaat gaaaaatact acttctttag cttgggctac  1890
atgtgtcagg gtttttctcc aggtgcttat attgatctgg aattgtaatg taaaaagcaa  1950
tgcaaactta ggcgagtact tcttgaaatg tctatttaag ctgctttaag ttaatagaaa  2010
agattaaagc aaaatattca tttttacttt ttcttatttt taaaattagg ctgaatgtac  2070
ttcatgtgat ttgtcaacca tagtttatca gagattatgg acttaattga ttggtatatt  2130
agtgacatca acttgacaca agattagaca aaaaattcct tacaaaaata ctgtgtaact  2190
atttctcaaa cttgtgggat ttttcaaaag ctcagtatat gaatcatcat actgtttgaa  2250
attgctaatg acagagtaag taacactaat attggtcatt gatcttcgtt catgaattag  2310
tctacagaaa aaaaatgttc tgtaaaatta gtctgttgaa aatgttttcc aaacaatgtt  2370
actttgaaaa ttgagtttat gtttgaccta aatgggctaa aattatatta gataaactaa  2430
aattctgtcc gtgtaactat aaattttgtg aatgcatttt cctggtgttt gaaaaagaag  2490
gggggagaa ttccaggtgc cttaatataa agtttgaagc ttcatccacc aaagttaaat  2550
agagctattt aaaaatgcac tttatttgta ctctgtgtgg cttttgtttt agaattttgt  2610
tcaaattata gcagaattta ggcaaaaata aaacagacat gtatttttgt ttgctgaatg  2670
gatgaaacca ttgcattctt gtacactgat ttgaaatgct gtaaatatgt cccaatttgt  2730
attgattctc tttaaatata aaatgtaaat aaaatattcc aat                    2773
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